

GenCore version 5.1.3							
Copyright (c) 1993 - 2003 Compugen Ltd.							
<b>OM protein - protein search, using sw model</b>							
Run on: February 12, 2003, 16:35:15 ; Search time 50 Seconds							
US-09-677-374-2							
Perfect score: 836	Score: 1	MNRGCLOGSLIISVPLVG.....IYGTACRQPDPGRWQVISTEK	Length: 162	Database: Swissprot_40:*	Number of hits satisfying chosen parameters: 112892	Total number of hits satisfying chosen parameters: 112892	Post-processing: Minimum Match 0%
Sequence: 1 MNRGCLOGSLIISVPLVG.....IYGTACRQPDPGRWQVISTEK 162							
<b>Scoring table:</b> BLOSUM62							
<b>Scoring table:</b> Gapop 10.0 , Gapext 0.5							
<b>Searched:</b> 112892 seqs, 4147628 residues							
<b>Total number of hits satisfying chosen parameters:</b> 112892							
Minimum DB seq length: 0	Maximum DB seq length: 200000000	Post-processing: Maximum Match 100%	Listing first 45 summaries	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
<b>Databse :</b> SUMMARIES							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
<b>ALIGNMENTS</b>							
Result No. Score Query Match Length DB ID Description							
1 296 35.4 159 1 17KD_RICPR P16621 rickettsia	RN [1] 17KD_RICPR	RP STANDARD;	PRT; 159 AA.				
2 294 35.2 159 1 17KD_RICJA P02763 rickettsia	RN [2] 17KD_RICJA	RP STRAIN=Madrid E;					
3 293 35.0 159 1 17KD_RICCN P05372 rickettsia	RX MEDLINE=9039499; PubMed=9823893;	RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,					
4 284.5 34.0 159 1 17KD_RICTY P22882 rickettsia	RA Scheinitz Ponten T., Alsmark U.C.M., Podowski R.M., Naezlund A.K.,	RA Eriksson A.-S., Winkler H.H., Kurland C.G.;					
5 284.5 33.0 154 1 17KD_RICAU P50927 rickettsia	RT "The genome sequence of Rickettsia prowazekii and the origin of	RT mitochondria.";					
6 263 31.5 154 1 17KD_RICAM P50930 rickettsia	RT mitochondrial DNA surface antigen precursor.	RT OMP OR RPB3.					
7 261 31.2 154 1 17KD_RICPA P50931 rickettsia	RT Rickettsiaceae; Rickettsiae; Rickettsiales;	RT NCBI_TaxID=782;					
8 261 31.2 154 1 17KD_RICRH P50929 rickettsia	RN [1] SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.					
9 258 30.9 154 1 17KD_RICMO P29697 rickettsia	RC STRAIN=Madrid E;	RC STRAIN=Madrid E;					
10 157 18.8 80 1 17KD_RICCA P31484 yersinia en CC	RC MEDLINE=80359171; PubMed=2768201;	RC Anderson B.E., Tzianabos T.;					
11 113.5 13.3 155 1 SYB_YEOLI CC	RT "Comparative sequence analysis of a genus-common rickettsial antigen gene.";	RT J. Bacteriol. 171:5199-5201(1989).					
12 105.5 12.6 155 1 SKB_SALTY CC	RT J. Bacteriol. 171:5199-5201(1989).	RT J. Bacteriol. 171:5199-5201(1989).					
13 105.5 12.6 155 1 SKB_HAEMIN CC	CC	CC					
14 102 12.2 155 1 PCP_HAEMIN CC	CC	CC					
15 99 11.8 179 1 YCFJ_ECOLI P37795 escherichia	CC	CC					
16 98 11.7 172 1 YGFH_ECOLI P76572 escherichia	CC	CC					
17 90 10.8 526 1 KCCJ_BOVIN P06391 bos taurus	CC	CC					
18 90 10.8 1332 1 XKDO_BACSU P54334 bacillus su	CC	CC					
19 89 10.6 1585 1 YOBO_BACSU P45931 bacillus su	CC	CC					
20 87.5 10.5 72 1 OSMB_SALTY P37723 salmonella	CC	CC					
21 86.5 10.3 72 1 OSMB_ECOLI P17873 escherichia	DR EMBL; M28482; AAA26378.1; ALT_SEQ.	DR EMBL; AJ235273; CAA15258.1; _					
22 84.5 10.1 243 1 CSH_SALTY P17853 salmonella	DR PIR; D33911; D33971.	DR PROTEIN; PS00013; PROKAR_LIPOPROTEIN; 1.					
23 84.5 10.1 301 1 SYTG_RAT P02138 rattus norv KW outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.	KW SIGNAL_	FT SIGNAL_					
24 84.5 10.1 431 1 KIB2_CANAL P00310 candida alb FT CHAIN_	FT CHAIN_	FT CHAIN_					
25 84.5 10.1 526 1 VP5_BTW1 P33476 bluetongue FT LIPID	FT CHAIN_	FT CHAIN_					
26 83.5 10.0 243 1 CSH_SALTI P082460 salmonella	FT LIPID	FT LIPID					
27 82 9.8 132 1 YEL15_AQUAE P066867 aquifex aeo FT N-ACYL DIGLYCERIDE (PROBABLE).	FT SEQUENCE	FT SEQUENCE					
28 82 9.8 263 1 CANS_BOVIN P13135 bos taurus SQ MW: A33D404B65EEB071 CRC64;	SQ	SQ					
29 81.5 9.7 541 1 NUS7_YEAST P48837 saccharomyces							
30 81.5 9.7 747 1 SDP1_NSPCL P19837 neptilia clia							
31 80.5 9.6 467 1 HEM1_MYCLET P46724 mycobacteri							
32 79.5 9.5 266 1 CANS_RABBIT P06813 oryctolagus							
33 79.5 9.5 359 1 ATPA_BOVIN P19482 bos taurus							



SO	SEQUENCE	159 AA:	142 EYTGACRQPDRQWQVIS
Query Match	35.0%; Score 293; DB 1; Length 159;	35.0%; Score 293; DB 1; Length 159;	35.0%; Score 293; DB 1; Length 159;
Best Local Similarity	38.1%; Pred. No. 1 3e-18;	38.1%; Pred. No. 1 3e-18;	38.1%; Pred. No. 1 3e-18;
Matches	61; Conservative 29; Mismatches 56; Indels 14; Gaps 4;	61; Conservative 29; Mismatches 56; Indels 14; Gaps 4;	61; Conservative 29; Mismatches 56; Indels 14; Gaps 4;
Oy	9 SSSLITISV--FLVGC-AQNSRQEYGAATGAVVGGVAGQLFGKGSRRVAMAIGAVLG 63	9 SSSLITISV--FLVGC-AQNSRQEYGAATGAVVGGVAGQLFGKGSRRVAMAIGAVLG 63	9 SSSLITISV--FLVGC-AQNSRQEYGAATGAVVGGVAGQLFGKGSRRVAMAIGAVLG 63
Db	5 SKIMITALAASMQACNPGMNCQGTGLGGAGGALLGSQFGKGKQLVGVGVALG 64	5 SKIMITALAASMQACNPGMNCQGTGLGGAGGALLGSQFGKGKQLVGVGVALG 64	5 SKIMITALAASMQACNPGMNCQGTGLGGAGGALLGSQFGKGKQLVGVGVALG 64
Oy	64 GLIGSKTQSMQDQDK---IKLNQSLERKVKAQGQVTRWRNPDTGNYSVEPVRYQRYNK 119	64 GLIGSKTQSMQDQDK---IKLNQSLERKVKAQGQVTRWRNPDTGNYSVEPVRYQRYNK 119	64 GLIGSKTQSMQDQDK---IKLNQSLERKVKAQGQVTRWRNPDTGNYSVEPVRYQRYNK 119
Db	65 AVLGGQIGAGMDEQDRRLAELTSQRALETAAPSGSNENVWRNPDTGNYGIVTPNKTY--- 119	65 AVLGGQIGAGMDEQDRRLAELTSQRALETAAPSGSNENVWRNPDTGNYGIVTPNKTY--- 119	65 AVLGGQIGAGMDEQDRRLAELTSQRALETAAPSGSNENVWRNPDTGNYGIVTPNKTY--- 119
Oy	120 QERROQCREFQQKAMTAGQKOEIYGTACRQPDPGRMOVIS 159	120 QERROQCREFQQKAMTAGQKOEIYGTACRQPDPGRMOVIS 159	120 QERROQCREFQQKAMTAGQKOEIYGTACRQPDPGRMOVIS 159
Db	120 RNSTGQYCERYTQTVVIGKQQKAYGNACRQPDPGQWQVVN 159	120 RNSTGQYCERYTQTVVIGKQQKAYGNACRQPDPGQWQVVN 159	120 RNSTGQYCERYTQTVVIGKQQKAYGNACRQPDPGQWQVVN 159
RESULT 4			
ID	17KD_RICRY STANDARD; PRT: 159 AA.		
AC	P22882;		
DT	01-AUG-1991 (Rel. 19, Created)		
DT	01-OCT-1991 (Rel. 19, Last sequence update)		
DE	17 kDa surface antigen precursor.		
GN	OMP.		
OS	Rickettsia australis.		
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiae; Rickettsia.		
OX			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Baird R. W., Ross B., Dwyer B.;		
RL	Submitted (OCT-1991) to the EMBL/Genbank/PDBJ databases.		
CC	- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).		
CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
CC			
CC	DR EMBL; M74042; AAA26394 1; -		
CC	DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.		
CC	KW Outer membrane; Lipoprotein; Antigen; Signal.		
FT	SIGNAL 1 19 BY SIMILARITY		
FT	CHAIN 20 >154 17 KDA SURFACE ANTIGEN.		
FT	LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).		
FT	NON_TER 154 154 . .		
SQ	SEQUENCE 154 AA: 15967 MW; E3AA833346FAC320 CRC64;		
Query Match	33.0%; Score 276; DB 1; Length 154;		
Best Local Similarity	38.1%; Pred. No. 3 6e-17;		
Matches	59; Conservative 27; Mismatches 55; Indels 14; Gaps 4;		
Oy	9 SSSLITISV--FLVGC-AQNSRQEYGAATGAVVGGVAGQLFGKGSRRVAMAIGAVLG 63		
Db	5 SKIMITALAASMQACNPGMNCQGTGLGGAGGALLGSQFGKGKQLVGVGVALG 64		
Oy	64 GLIGSKTQSMQDQDK---IKLNQSLERKVKAQGQVTRWRNPDTGNYSVEPVRYQRYNK 119		
Db	65 AVLGGQIGAGMDEQDRRLAELTSQRALETAAPSGSNENVWRNPDTGNYGIVTPNKTY--- 123		
Oy	120 QERROQCREFQQKAMTAGQKOEIYGTACRQPDPGR 154		
Db	124 ---GQCRCYTVVIGKQQKAYGNACRQPQG 154		
RESULT 6			
ID	17KD_RICAM STANDARD; PRT: 154 AA.		
AC	P20927;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DE	17 kDa surface antigen precursor (Fragment).		
GN	OMP.		
OS	Rickettsia amblyommi.		
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiae; Rickettsia.		
OX			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MO 85-1084.		



RESULT 9  
 17KD\_RICMO STANDARD; PRT; 154 AA.  
 ID -17KD\_RICMO STANDARD; PRT; 154 AA.  
 AC P50929;  
 DT 01-OCT-1995 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE 17 kDa surface antigen precursor (Fragment).  
 GN Rickettsia montana.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OC NCBI\_TaxID=33991;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Ohio 83-441;  
 RC Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.;  
 RC Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).

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DR EMBL; M82879; -; NOT\_ANNOTATED\_CDS.  
 DR InterPro; IPR00417; Prok\_lipoprot.  
 DR PROSITE; PS0013; PROKAR\_LIPOPROTEIN; PARTIAL.  
 CC KW Outer membrane; Lipoprotein; Antigen.  
 CC FT NON\_TER 1 1  
 CC FT NON\_TER 80 80  
 CC SQ SEQUENCE 80 AA; 8372 MW; AD289A48EAB19E0E CRC64;

Query Match 18.8%; Score 157; DB 1; Length 80;  
 Best Local Similarity 40.3%; Pred. No. 3.5e-07;  
 Matches 31; Conservativeness 15; Mismatches 27; Indels 4; Gaps 1;  
 Qy 9 SSLITIV--FLVGC--AQNSRQEVAATGAWVGCGAVAGQLFGKGSGRGRAMAIGGAVL 63  
 Db 5 SKIMTIALAASMLQACNGPQGMNKQGTGTLGGAGGALLGSOFQGOKGKGOLVGVGALL 64  
 Qy 64 GLISGIQGSMQDK--IKLNQSLEKKVAKAGQVFRWRNPDTGNSVSVEPVRYTYRN 119  
 Db 65 AVLGGIGAGMDEQDRRLAEATSQRALETPSGSNVEMWRNPFDNGNYGYVTPNKTY --- 119  
 Qy 120 QERRQYCRCERQQAKMTAGQKQKETYGTACROPDG 154  
 Db 120 RNSTGOVCRETYQTWVIGGKOKAYGIAACLOPDGQ 154

RESULT 10  
 17KD\_RICCA STANDARD; PRT; 80 AA.  
 ID -17KD\_RICCA STANDARD; PRT; 80 AA.  
 AC P29697;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE 17 kDa surface antigen (Fragment).  
 GN Rickettsiaceae.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OC NCBI\_TaxID=788;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 MEDLINE-#21089; PubMed=1732192;  
 RC STRAIN=ATCC 51872 / WA-C / Serotype O:8;  
 RC MEDLINE-#2121089; PubMed=1732192;  
 RA Baeumler A.J.; Hantke K.;  
 RT "A lipoprotein of *Yersinia enterocolitica* facilitates ferrioxamine uptake in *Escherichia coli*.";  
 RT J. Bacteriol. 174:1029-1035(1992).  
 CC -!- FUNCTION: FACILITATES FERRIOXAMINE UPTAKE.  
 CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor.  
 CC -!- SIMILARITY: TO *E. coli* AND *S. TYPHIMURIUM* SLYB AND TO *H. INFLUENZAE* FCP.

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DR EMBL; X00448; CAA29771; -.





Best Local Similarity 39.6%; Pred. No. 0.038; Matches 21; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

Oy 30 VGAATGAVVGGVAGQFLGKSSGRVAMAIGGAVLGLIGSKIGSQMDQQKIKL 82  
 ||| | :||| | :||| :||| :||| :||| :|||  
 Db 62 VGTLLGGALGGIAGSRTIGGRQATAAIVVGAIGGAGIAGSKIEERNSQVNQAEI 114

RESULT 15  
 YCFJ\_ECOLI STANDARD PRT: 179 AA.

AC P37795; P5951;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein ycfj.  
 GN YCFJ OR B110.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID:562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Kamio K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Niishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horinuchi T.;  
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155(1996).  
 RN [3]  
 RP SEQUENCE OF 1-63 FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=81236546; PubMed=6265208;  
 RA Young J.G., Rogers B.L., Campbell H.D., Jaworowski A., Shaw D.C.;  
 RT "Nucleotide sequence coding for the respiratory NADH dehydrogenase of  
 RT Escherichia coli. Trig initiation codon.";  
 RL Eur. J. Biochem. 116:165-170(1981).  
 RN [4]  
 RP IDENTIFICATION  
 RX MEDLINE=95075659; PubMed=7984428;  
 RA Borodovsky M., Rudd K.E., Koonin E.V.;  
 RT "Intrinsic and extrinsic approaches for detecting genes in a  
 bacterial genome.";  
 RL Nucleic Acids Res. 22:4756-4767(1994).  
 CC NUCLEIC ACIDS RES.: TO RICKETTSIA 17 kDa SURFACE ANTIGEN  
 CC  
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 CC  
 DR EMBL; AE00211; AAC74194.1; -  
 DR EMBL; D9746; BAA35925.1; -  
 DR EMBL; V00306; -; NOT\_ANNOTATED\_CDS.  
 DR EcoGene; EG12444; ycfj.

KW HYPOTHETICAL PROTEIN; TRANSMEM 5; POTENTIAL.  
 FT 179 AA; 18920 MW; BA5EB0DB5CD45609 CRC64;  
 SEQUENCE

Query Match Best Local Similarity 11.8%; Score 99; DB 1; Length 179;  
 Matches 26; Conservative 12; Mismatches 32; Indels 26; Gaps 1;

Oy 31 GAATGAVVGGVAGQFLGKSSGRVAMAIGGAVLGLIGSKIGSQMDQQKIKLNSLEKV 90  
 ||| | :||| | :||| :||| :||| :||| :||| :|||  
 Db 73 GSVLGAVAGVGVIGHOFGGGRGKDVTVGALGGYAGNOLQGSLOED----- 120  
 Oy 91 AGQVTRWRNPDIIGNSYSEPVRYIQRNQERRQY 126  
 ||| | :||| | :||| :||| :||| :|||  
 Db 121 -----TYTTQORCKTVVDKSERNLGY 142  
 Search completed: February 12, 2003, 16:44:11  
 Job time : 52 secs



C;Species: Rickettsia conorii  
 C;Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 20-Aug-1999  
 C;Accession: B33971  
 R;Anderson, B.E.; Tzianabos, T.  
 J;Bacteriol. 171, 5199-5201, 1989  
 A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.  
 A;Reference number: A33971; MUID:89359171; PMID:2768201  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-159 <AND>  
 C;Cross-references: GB:MR28479; NID:9152463; PIDN:AAA26379.1; PID:9152464  
 C;Superfamily: rickettsial common antigen  
 Query Match 35.0%; Score 293; DB 2; Length 159;  
 Best Local Similarity 38.1%; Pred. No. 1 2e-18; Indels 14; Gaps 4;  
 Matches 61; Conservative 29; Mismatches 56; Indels 14; Gaps 4;  
 QY 9 SSLIITSV--FLVGC-AQNFSSRVEGANTGAVVGGVAGOLFKGKGSGRVAMAIAGAVLG 63  
 | :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||:  
 Db 5 SKIMILATSMIQLACNGPGGMNKQGTGTLGGAGALLSGSFGKGKGQLVGVGQGALLG 64  
 QY 64 GLIGSKTGSMDQDK---IKLNQSLERVKAGQVTRWRNPDTGNSYSVERVTYQRYNK 119  
 ::| :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||:  
 Db 65 AVLGGQIGAGMDEQDRRLAELTSORALETAPSGSNVERWNPDPNGNYVTPNKT----- 119  
 QY 120 QERRQQCEREFOOKAMTAGQKQETYACRQPDGQWVIS 159  
 :| |||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||:  
 Db 120 RNSTGOYCERYTOTVVIGGKOKAYGNACRQPDGQWVN 159

RESULT 3  
 A33971  
 Rickettsial common antigen precursor - Rickettsia rickettsii  
 C;Species: Rickettsia rickettsii  
 C;Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 20-Aug-1999  
 C;Accession: A33971  
 R;Anderson, B.E.; Tzianabos, T.  
 J;Bacteriol. 171, 5199-5201, 1989  
 A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.  
 A;Reference number: A33971; MUID:89359171; PMID:2768201  
 A;Accession: A33971  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-159 <AND>  
 A;Cross-references: GB:MR28480; NID:9152457; PIDN:AAA26376.1; PID:9152458  
 C;Superfamily: rickettsial common antigen  
 Query Match 35.0%; Score 293; DB 2; Length 159;  
 Best Local Similarity 38.1%; Pred. No. 1.2e-18; Indels 14; Gaps 4;  
 Matches 61; Conservative 29; Mismatches 56; Indels 14; Gaps 4;  
 QY 9 SSLIITSV--FLVGC-AQNFSSRVEGANTGAVVGGVAGOLFKGKGSGRVAMAIAGAVLG 63  
 | :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||:  
 Db 5 SKIMILATSMIQLACNGPGGMNKQGTGTLGGAGALLSGSFGKGKGQLVGVGQGALLG 64  
 QY 64 GLIGSKTGSMDQDK---IKLNQSLERVKAGQVTRWRNPDTGNSYSVERVTYQRYNK 119  
 ::| :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||:  
 Db 65 AVLGGQIGAGMDEQDRRLAELTSORALETAPSGSNVERWNPDPNGNYVTPNKT----- 119  
 QY 120 QERRQQCEREFOOKAMTAGQKQETYACRQPDGQWVIS 159  
 :| |||: | :|||: | :|||: | :|||: | :|||: | :|||:  
 Db 120 RNSTGOYCERYTOTVVIGGKOKAYGNACRQPDGQWVN 159

RESULT 5  
 C33971  
 Rickettsial common antigen precursor - Rickettsia typhi  
 C;Species: Rickettsia typhi  
 C;Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 20-Aug-1999  
 C;Accession: C33971  
 R;Anderson, B.E.; Tzianabos, T.  
 J;Bacteriol. 171, 5199-5201, 1989  
 A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.  
 A;Reference number: A33971; MUID:89359171; PMID:2768201  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-159 <AND>  
 A;Cross-references: GB:MR28481; NID:9152459; PIDN:AAA26377.1; PID:9152460  
 C;Superfamily: rickettsial common antigen  
 Query Match 34.0%; Score 284.5; DB 2; Length 159;  
 Best Local Similarity 39.9%; Pred. No. 7e-18; Indels 49; Gaps 9; Gaps 2;  
 Matches 55; Conservative 25; Mismatches 49; Indels 9; Gaps 2;  
 QY 26 SRQEVGAAATGAVVGGVAGOLFKGKGSGRVAMAIAGAVLG 81  
 | :|||: | :|||: | :|||: | :|||: | :|||: | :|||: | :|||:  
 Db 27 NKQGTTGTLGGAGGAGLGSFGKGKGQLVGVGQGALLGAVLGGQGASLDEQDRKLEI 86  
 QY 82 DNQSLERVKAGQVTRWRNPDTGNSYSVERVTYQRYNKQRRQQCEREFOOKAMTAGOKO 141  
 ::| :|||: | :|||: | :|||: | :|||: | :|||: | :|||:  
 Db 87 SQRALESAPSGSNVERWNPDPNGNYVTPNKT-----RNSTGOYCERYTOTVVIGGKQ 141  
 QY 142 EYTGACRQPDGQWVIS 159  
 || :|||: | :|||: | :|||:  
 Db 142 TYTGACRQPDGQWVN 159

RESULT 6  
 A25972  
 17K antigen precursor - Rickettsia rickettsii  
 C;Species: Rickettsia rickettsii  
 C;Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 20-Aug-1999  
 C;Accession: A25972  
 R;Anderson, B.E.; Regnery, R.L.; Carbone, G.M.; Tzianabos, T.; McDade, J.B.E.; Fu, Z.Y.  
 J;Bacteriol. 169, 2385-2390, 1987  
 A;Title: Sequence analysis of the 17-kilodalton antigen gene from Rickettsia ricketts  
 A;Reference number: A25972; MUID:87222152; PMID:3108232  
 A;Accession: A25972

RESULT 4  
 G97860  
 17K surface antigen precursor [imported] - Rickettsia conorii (strain Malish 7)  
 C;Species: Rickettsia conorii  
 C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 22-Oct-2001  
 C;Accession: G77860  
 R;ogata, H.; Adic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; RC  
 Science 293, 2093-2098, 2001

A; Molecule type: DNA  
A; Residues: 1-159 <AND>  
A; Cross-references: GB:ML6486; NID:9152467; PIDN:AAA26081.1; PID:9152468  
C; Superfamily: rickettsial common antigen

Query Match 34.0%; Score 284; DB 2; Length 159;  
Best Local Similarity 37.5%; Pred. No. 7.7e-18; Mismatches 57; Indels 14; Gaps 4;  
Matches 60; Conservative 29; Mismatches 57;

Qy 9 SSLIISV--FLVGC--AQNSRQEVAATGAVVGGVAGOLFKGSGRVAAMIGAVLG 63  
Db 5 SKIMILATLSMQLACNGPGMMKQGTGAGGALLSOFGGKGQLVGVCGALG 64

Qy 64 GLIGSKTGQSMDQDK----TKLNQSLKEVKVAGQVTRWRNRDGTGSYSVERVTORYNK 119  
Db 65 AVLGGQGIGAGMDEQDRRLAELTSQRALLETAPSMSGNVWERNFDNGNYGYVIPNKT----- 119

Qy 120 QBRROOYCREFOOKAMIAQOKOEIYGTACROPPDGKQHVIS 159  
Db 120 RNSTGQYCREYQTQVVIGGKQOKAYGDACROPDEQMVVN 159

RESULT 7

DB3169 conserved hypothetical protein PA3819 [imported] - Pseudomonas aeruginosa (strain PA01)  
C; Species: Pseudomonas aeruginosa  
C; Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 01-Mar-2002  
C; Accession: DB3169  
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.T.; Coulter, S.N.; Folger, K.R.; Kas, A.; Labbig, K.; Ljim, L.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A; Reference number: A82950; MUID:20437337; PMID:10984043  
A; Accession: DB3169  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-182 <STO>  
A; Cross-references: GB:AE004799; GB:AE004091; NID:99949981; PIDN:AAG07206.1; GSPDB:GN001  
A; Experimental source: strain PA01  
C; Genetics:  
A; Gene: PA3819  
C; Superfamily: PAL cross-reacting lipoprotein

Query Match 15.4%; Score 128.5; DB 2; Length 182;  
Best Local Similarity 34.8%; Pred. No. 0.0004; Mismatches 32; Conservative 13; Mismatches 28; Indels 19; Gaps 2; Matches 32;

Qy 28 QBYGANTGAVVGGVAGOLFKGSGRVAAMIGAVLGGLIGKIGQSMQDQKI----- 80  
Db 70 QIAGTAIGAVVGGLGNQIGGGKKITAVGAGVGGYAGNKVQEGMQERDTYTTETRC 129

Qy 81 -KLKNQSLKEV-----KAGOTWRWNP 100  
Db 130 STVHDSSKEVVGVDVKYMLDGKAGQIRMEDP 161

RESULT 8

AT3418 17K surface antigen precursor [imported] - Brucella melitensis (strain 16M)  
C; Species: Brucella melitensis  
C; Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
C; Accession: AT3418  
R; DelVecchio, V.G.; Kaparla, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goetsman, E.; Sejkov, B.; Elzer, P.H.; Hagiwara, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A; Reference number: AD3252; PMID:11756688  
A; Accession: AT3418  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-131 <KUR>  
A; Cross-references: GB:AE008917; PIDN:AAL52516.1; PID:917983328; GSPDB:GN0190

A; Experimental source: strain 16M  
C; Genetics:  
A; Gene: BMEL1335  
A; Map position: I

Query Match 15.0%; Score 125.5; DB 2; Length 131;  
Best Local Similarity 31.7%; Pred. No. 0.00052; Mismatches 39; Conservative 18; Mismatches 43; Indels 23; Gaps 7; Matches 39;

Qy 47 GKGSGRVAMAATGG-----AVIG-GLIGSKIQ---SMQQDKIKLNQSLEKVKAG 92  
Db 14 GKGS---FP\$GGSSOKPTEVNLASIGNLGERNSAQLSADRRALEAFRAYESPAQ 71

Qy 93 QVTRWRNRDTONSYSEPVRYTORYNQERKQOCREFOOKAMIAQOKOEIYGTACRQPD 152  
Db 72 KSVLWSGAGS-NAGDVTAAQPIO-----VGSONCRQYSHSFTIGGDOQIVRGTAGRNP 124

Qy 153 GRW 155  
Db 125 GSW 127

RESULT 9

BB3514 conserved hypothetical protein PA1053 [imported] - Pseudomonas aeruginosa (strain PA01)  
C; Species: Pseudomonas aeruginosa  
C; Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C; Accession: BB3514  
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.T.; Coulter, S.N.; Folger, K.R.; Kas, A.; Labbig, K.; Ljim, L.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A; Reference number: A82950; MUID:20437337; PMID:10984043  
A; Accession: BB3514  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-154 <STO>  
A; Cross-references: GB:AE04537; GB:AE004091; NID:99946960; PIDN:AAG0442.1; GSPDB:GN001  
A; Experimental source: strain PA01  
C; Genetics:  
A; Gene: PA1053  
C; Superfamily: PRL cross-reacting lipoprotein

Query Match 13.9%; Score 116; DB 2; Length 154;  
Best Local Similarity 25.0%; Pred. No. 0.0042; Mismatches 34; Conservative 21; Mismatches 41; Indels 40; Gaps 3; Matches 34;

Qy 1 MRNGCLOGSSLITISPLVGC-----AQNFSRQE----- 29  
Db 1 MRKSALTIVASPTAMALAGGCGSSLGDTYSERAVTIVTRVMGTOIALRRPVKIEGKTTP 60

Qy 30 VRATGAVVGGVAGOLFKGSGRVAAMIGAVLGGLIGSKIQSMQDQDKL----- 82  
Db 61 IGSIAKGKVGVGAGSAVGGGKGSYVAATIGAVAGGILGAATTEEGLRTQGEVITVREDDG 120

Qy 83 --NOSLEKVKQGVTR 96  
Db 121 STRAYVQDVQDQIFR 136

RESULT 10

S23787 outer membrane lipoprotein precursor - Yersinia enterocolitica  
C; Species: Yersinia enterocolitica  
C; Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 29-Sep-1999  
C; Accession: S23787  
R; Baumberger, A.J.; Hantke, K.  
J. Bacteriol. 174, 1029-1035, 1992

A; Title: A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in  
A; Reference number: S23786; MUID:92121089; PMID:1732192  
A; Accession: S23787  
A; Status: preliminary

A; Molecule type: DNA  
 A; Residues: 1-155 <R>  
 A; Cross-references: EMBL:X60448; NID:948577; PIDN:CAA42977.1; PID:948579  
 C; Superfamily: PAL cross-reacting lipoprotein

Query Match Best Local Similarity 13.6%; Score 113.5; DB 2; Length 155; Matches 37; Conservative 19; Mismatches 43; Indels 51; Gaps 4;

QY 10 SLITISVFLVGCAQN-----FQRQE-----  
 Db 7 AVAIAVATLNGCANNLTSGDVFASQAKOVTVTYGTLISVRPTILOGGDDNNVMAG 65  
 QY 35 GAVNVGVAGOLFCKGSGRVAMAIGAVNLGLIGKIGSMDQDKIKL----- 34  
 Db 67 GAVIGGFLGNTVGGTGRSLATAAGAVAGGMAQGQVQGMNRIDGVQLEVRKDGTILV 126  
 QY 83 -NQSLEKKKAGQVTRWRNPDTGNNSYSVP 110  
 Db 127 VQKQGPTRFSVQG--RVMLASSGSSIVTVSP 154

RESULT 11

B82837 conserved hypothetical protein Xf0178 [imported] - *Xylella fastidiosa* (strain 9a5c)  
 C; Species: *Xylella fastidiosa*  
 C; Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C; Accession: B82837  
 R; anonymous. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000  
 A; Title: The genome sequence of the Plant pathogen *Xylella fastidiosa*.  
 A; Reference number: A825155; MUID:20365717; PMID:10910347  
 A; Note: for a complete list of authors see reference number A59328 below  
 A; Accession: B82837  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-257 <SIM>  
 A; Cross-references: GB:AE003872; GB:AE003849; NID:9104975; PIDN:AAF82991.1; GSPDB:GN001  
 A; Experimental source: strain 9a5c  
 R; Simpson, A.J.G.; Reinach, F.C.; Abreu, F.A.; Aencio, M.; Alfarenga, R.; As-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, J.A.S.  
 Submitted to GenBank, June 2000  
 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohn, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laigrado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.; Martins, E.M.F.; Matos, A.Y.; Menck, C.F.M.; Miracola, E.C.; Miyaki, C.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; Rodriques, V.; Rosa, A.J.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsukako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zilberman, S.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McClellan, R.; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Karp, P.; Romero, P.; Zhang, S.

Query Match Best Local Similarity 13.3%; Score 111.5; DB 2; Length 142; Matches 41; Conservative 21; Mismatches 60; Indels 29; Gaps 9;

Db 10 SLIIISVFLVGCAQNFSRQEVAIGAVVGGVAGQLFGKGSGRVAMAIGAVNLGLIGSK 69  
 Db 12 STLCVSM-LSAC-----TTTCTRPAG-GSLEFR-SAQPSTPFLANLQGIVG-K 56  
 QY 70 ICQSMSMDQDKIKL---NQSLEKKVAGQVTRWRNPDT-GNSYSVERPVRYQYKQERQ 124  
 Db 57 SVEVLQRGDQTAKALEREYKALETAPVGTPVWTGDDVKGQVWANAP---YOGVN---- 107  
 QY 125 QYCREFOQKAMIAQOQEIQTGACROPDPGRW 155  
 Db 108 QNCROQYSHTLTVGDGRTRVRAACRNDDGSW 138

RESULT 13

D97478 lipa protein [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)  
 C; Species: *Agrobacterium tumefaciens*  
 C; Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
 R; Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, A.; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium* J. D.; Reference number: A973559; PMID:11743194  
 A; Accession: D97478  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-125 <RUR>  
 A; Cross-references: GB:AE007869; PIDN:AAK86781.1; PID:gi15155981; GSPDB:GN00169  
 A; Gene: ACR\_C\_1782  
 A; Map position: circular chromosome

Query Match Best Local Similarity 13.3%; Score 111; DB 2; Length 125; Matches 36; Conservative 18; Mismatches 61; Indels 16; Gaps 6;

QY 30 VGAATGAVVGGVAGOLFCKGSGRVAMAIGAVNLGLIGKIGSMDQDKIKL---NQS 85  
 Db 2 LSACTTGTGPRAGSSLFGR-SAOGSTPFLANLQGIVG-KSGVELDRDQTALEIYKA 59  
 QY 86 LEKVKAGQVTRWRNPDT-GNSYSVERPVRYQYKQERQQCREFEFOQKAMIAQOEIY 144  
 Db 60 LETAVGTPVWTGDDVKGQVWANAP---YOGVN----QNCROQYSHTLTVGDGRTRV 110  
 QY 145 GTACRQPDGRW 155

RESULT 12

AD2696 lipa protein [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)  
 C; Species: Agrobacterium tumefaciens  
 C; Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C; Accession: AD2696  
 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McClellan, R.; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McClellan, R.; Karp, P.; Romero, P.; Zhang, S.

RESULT 14

S58334 lipa protein - *Rhizobium leguminosarum*

C;Species: *Rhizobium leguminosarum*  
 C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
 C;Accession: S58234  
 R;Yeoman, K.H.; Delgado, M.J.; Downie, J.A.; Johnston, A.W.B.  
 submitted to the EMBL Data Library, July 1995

A;Reference number: S58232

A;Accession: S58234

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-139 <YEC>

A;Cross-references: EMBL:X89983; NID:929821; PIDN:CAA62010.1; PID:929824

Query Match	Score	DB	Length
Best Local Similarity	13.3%	2	139
Matches	25.2%	Pred. No.	0.01
Matches	38	Mismatches	18
		Indels	30
		Gaps	6
Qy	10	SU11SVFLVGCAQNFSRQEVAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLGSK	69
Db	11	SALLALVALSGCTTTSASR-----GIFSSKPSASAFT- ALQGIVG-R	54
Qy	70	IGOSMDQDKIKL---NOSLEKVAGQVTRWRNPDT-GTNSYSVEPVRTYQRYNKERO	124
Db	55	SGVSLTDSDKQRALEATEYRALEGAVGQPVLTGKDVTKVVAAPYOV-----GS	105
Qy	125	QYCREFQOKAMTAGQKOEIYGACRQPDPGRW	155
Db	106	QNCRQYHTLTVDGKDTVARGAACRNNDGSW	136

### RESULT 15

g87629 hypothetical protein CC3073 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C;Accession: G87629

R;Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonowich, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98: 4135-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: G87629

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-232 <STO>

A;Cross-references: GB:AE005673; NID:913424723; PIDN:AAK25035.1; GSPDB:GN00148

C;Genetics:

C;Gene: CC3073

Query Match	Score	DB	Length
Best Local Similarity	13.2%	2	232
Matches	26.9%	Pred. No.	0.02
Matches	43	Mismatches	22
		Indels	56
		Gaps	39
			5

Qy	18	LYGCQAQNFSRQEVGAVGAVVGGVAGQLFGK---GGSRVAMAIGGAVLGGLGSKIGQSM	74
Db	81	VVGCKA\$GKQEVGVAVVGGALIGAAGAAGSNLAKNQDGCTGAIGAVVAGAGSLLGCKMQSKD	140
Qy	75	DODDKIKLNQS-----LEVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKOE	121
Db	141	AAQEVGGLYKSGFRYQTQAPLVIKEKKR-----STVNL-----	180
Qy	122	RROQYCREFQOKAMIAQOKQEQTYGTACRQPDRWQVISTE	161
Db	181	RAA\$TRGERLGAVIDSCTTFQALG--RTKOCKWILVGQD	217

Search completed: February 12, 2003, 16:45:57  
 Job time : 55 secs

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GenCore version 5.1.3  
copyright (c) 1993 - 2003 Compugen Ltd.

## Om protein - protein search, using sw model

Run on: February 12, 2003, 16:34:58 ; Search time 36 Seconds

(without alignments)  
599.628 Million cell updates/sec

Title: US-09-677-374-2

Perfect score: 1 MNRGCLQGSLLIISVFLVG... IYGTACRQPDRMQVISTER 162

Sequence: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:

908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002,\*  
1: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1980.DAT: \*  
2: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1981.DAT: \*  
3: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1983.DAT: \*  
4: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1984.DAT: \*  
5: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1985.DAT: \*  
6: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1986.DAT: \*  
7: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1987.DAT: \*  
8: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1988.DAT: \*  
9: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1989.DAT: \*  
10: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1990.DAT: \*  
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22: /SIDS2/gcadata/geneseq/geneseq -emb1/AA2002.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	836	100.0	162 22	AAG78025
2	836	100.0	162 22	AAB81126
3	836	100.0	162 23	AAB91867
4	815	97.5	161 22	AAB81127
5	815	97.5	161 23	AAB7868
6	815	97.5	256 22	AAB81128
7	815	97.5	256 23	AAB91869
8	112	13.4	20 22	AAB81130
9	112	13.4	20 22	AAU97871
10	112	13.4	23 23	AAO17565

## ALIGNMENTS

RESULT 1	AAG78025	ID AAG78025 standard; Protein: 162 AA.
	X	AC AAG78025;
	X	DT 15-JAN-2002 (first entry)
	X	DE Piscirickettsia salmonis polypeptide P10.6.
	X	KW Piscirickettsia salmonis; Piscirickettsiosis; salmonid rickettsial; septicemia; SRS; surface antigen; vaccine; antibacterial; fish; ATCC VR-1361.
	X	OS Piscirickettsia salmonis.
	X	PN WO200168865-A2.
	PD 20-SEP-2001.	
	XX	PP 12-MAR-2001; 2001WO-GB01055.
	XX	PR 11-MAR-2000; 2000GB-0005838.
	PR 01-JUL-2000; 2000GB-0016082.	
	PR 29-JUL-2000; 2000GB-0018599.	
	XX	(AQUA-) AQUA HEALTH EURO LTD.
	XX	PI Simard N, Brouwers H, Jones S, Griffiths S, Valenzuela P;
	PI Burzio L;	
	XX	WPI; 2001-639050/73.

DR N-PSDBB; AAH79040.

XX

PT

New nucleic acids encoding an amino acid sequence homologous to the

PT

surface antigen present on *Piscirickettsia salmonis* are useful to

PT

protect fish against piscirickettsiosis -

XX

PS Claim 6; Fig 5; 25pp; English.

XX

CC

The invention relates to nucleic acid sequences and the encoded protein

CC

of a least part of the surface antigen present on *Piscirickettsia*

CC

salmonis for production of a vaccine with antibacterial activity to

CC

protect fish against *P. salmonis* which causes piscirickettsiosis, also

XX

CC

known as salmonid rickettsial septicaemia.

SQ Sequence 162 AA;

SO

Query Match

Best Local Similarity

100.0%

Score

836;

DB

22;

Length

162;

Matches

162;

Conservative

0;

Pred.

No.

3;

8e-80;

Gaps

0;

Indels

0;

Matches

162;

Mismatches

0;

Gaps

0;

Indels

0;

Matches

162;

Conservative

0;

Pred.

No.

3;

8e-80;

Gaps

0;

Indels

0;

Query

1 MNRGCLQGSLLITISVFLVGCAONFSRQEVGAATGAVWGGVAGLPGKGSGRVANAGGA 60

Db

1 MNRCGLQGSLLITISVFLVGCAONFSRQEVGAATGAVWGGVAGLPGKGSGRVANAGGA 60

Oy

61 VLGGILGSKIGQSMQDQDKIKLNQSLEKVKAGQVTRWRNPDGTGNSYSVEVRTYQRNKQ 120

Db

61 VLGGILGSKIGQSMQDQDKIKLNQSLEKVKAGQVTRWRNPDGTGNSYSVEVRTYQRNKQ 120

Oy

- 121 ERROQYCREFQKAMIQAGQKQPIYGACRODPGRMVISTEK 162

Db

121 ERROQYCREFQKAMIQAGQKQPIYGACRODPGRMVISTEK 162

Oy

RESULT 2

AAB81125

ID

AAB81126 standard; Protein; 162 AA.

XX

AC

AAB81126;

XX

'DT

11-JUL-2001 (first entry)

XX

DE

OSPA antigen amino acid sequence.

XX

KW

Poikilothermic fish; *Piscirickettsia salmonis*; rickettsial pathogen; SRS.

XX

KW

vaccine; OSPA; salmonid rickettsial septicaemia; rickettsial disease;

XX

OS

*Piscirickettsia salmonis*.

XX

KW

Key

Location/Qualifiers

FT

110..129

/label=B-cell-epitope

XX

XX

CA2281913-A1.

XX

XX

PD

17-MAR-2001.

XX

PP

17-SEP-1999; 99CA-2281913.

XX

PR

17-SEP-1999; 99CA-2281913.

XX

PA

(KAYW/) KAY W W.

PA

(BURI/) BURIAN J.

PA

(KUZY/) KUZYK M A.

XX

PT

Kay WW, Burian J, Kuzyk MA;

XX

PT

WPI; 2001-316844/34.

DR

N-PSDB; AAF81246.

XX

XX

PS

Example 2; Fig 2B; 35pp; English.

XX

PS

This invention relates to a method for the protection against infection

CC

XX

PS

Outer surface lipoprotein; OSPA; antibacterial; immunosuppressive; Rickettsial disease.

XX

XX

DE

Piscirickettsia salmonis outer surface lipoprotein Ospa.

XX

KW

vaccine; poikilothermic fish; fin-fish; Rickettsial septicemia;

XX

OS

*Piscirickettsia salmonis*.

XX

PN

CA23939327-Al.

XX

PD

15-MAR-2002.

XX

PF

19-MAR-2001; 2001CA-2339327.

XX

PR

15-SEP-2000; 2000US-0677374.

XX

PA

(THOR/) THORNTON J C.

PA

(KAYW/) KAY W W.

PA

(BURI/) BURIAN J.

PA

(KUZY/) KUZYK M A.

PA

(KUZY/) KUZYK M A.

PA

WPI; 2002-455221/49.

XX

PT

Thornton JC, Kay WW, Burian J, Kuzyk MA;

XX

DR

WPI; 2002-455221/49.

XX

DR

N-PSDB; AAK5201.

XX

PT

Inducing immunity in fin fish to Rickettsial septicemia, comprises

PT

administration of an outer surface lipoprotein (ospa) of a bacterial

XX

PS

Claim 15; Fig 2; 55pp; English.

XX

The invention describes a method of protecting a Poikilothermic fish comprising infection by the bacterial pathogen *Piscirickettsia salmonis* orally, an immunogenic amount of principal antigen, the Ospa (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (Ospa) of bacterial strain *Piscirickettsia salmonis* as a vaccine to induce immunity in fin-fish against Rickettsial septicæmia and other related Rickettsial diseases caused by either a virus, bacteria or parasite.

This is the amino acid sequence of the *Piscirickettsia salmonis* outer surface lipoprotein, Ospa, used in the creation of the vaccine described in the invention.

XX  
SQ Sequence 162 AA;

Query Match 100 %; Score 816; DB 23; Length 162;

Best Local Similarity 100.0%; Pred. No. 3. 8e-80;

Matches 162; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Oy 1 MNRGCLOGSSLISLIVSFLVGAQNSFROEVGAATGAVVGGVASOLFQKGSGRVAMAIAGA 60

Db 1 MNRGCLOGSSLISLIVSFLVGAQNSFROEVGAATGAVVGGVASOLFQKGSGRVAMAIAGA 60

Oy 61 VLGGLGSKIGOSMDODDKIKLNQSEKVKAGQTWRNRPDTGNNSYSEPVRTYORYNKO 120

Db 61 VLGGLGSKIGOSMDODDKIKLNQSEKVKAGQTWRNRPDTGNNSYSEPVRTYORYNKO 120

Oy 121 ERQQYCREFQQAKMAGOKOETIYTACQPDGKQVISTEK 162

Db 121 ERQQYCREFQQAKMAGOKOETIYTACQPDGKQVISTEK 162

RESULT 4

AABB1127

ID ABB1127 standard: Protein: 161 AA.

XX

AC

DE

DT

XX

DE

Optimised Ospa protein 17E2 amino acid sequence.

XX

KW

Polikithermic fish; *Piscirickettsia salmonis*; rickettsial pathogen; vaccine; Ospa; salmonid rickettsial septicæmia; rickettsial disease; SRS.

XX

OS

Piscirickettsia salmonis.

OS

Synthetic.

XX

FH

Key

FT

Region

106..128

/label= B\_cell\_epitope

XX

PN

CA2281913-A1.

XX

PD

17-MAR-2001.

XX

PF

17-SEP-1999;

99CA-2281913.

XX

PR

17-SEP-1999;

99CA-2281913.

XX

(KAYW/) KAY W W.

PA (BURJ/) BURIAN J.

PA (KUZY/) KUZYK M A.

XX

PI

Kay WW,

Burian J,

Kuzyk MA;

XX

DR

N-PSDB; ABK86247.

XX

PT

Method for protecting poikilothermic fish against salmonid rickettsial

PT

vaccine containing the Ospa protein of *Piscirickettsia salmonis*

XX

PS

Disclosure: FIG 5; 35PP; English.

This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, *Piscirickettsia salmonis*. The method comprises administering an immunogenic amount of a *P. salmonis* specific antigen termed Ospa, or an immunogenic fragment of Ospa in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen *P. salmonis*. The method is also useful for protecting against salmonid rickettsial septicæmia (SRS) and other rickettsial diseases. The present sequence represents optimised *P. salmonis* Ospa protein 17E2. The DNA encoding Ospa 17E2 (AAF66247) has been optimised for expression in *Escherichia coli*. An Ospa protein with an N-terminal fusion partner is used in a vaccine to create an anti-Ospa antibody response.

XX

SQ Sequence 161 AA;

XX

Query Match 97.5%; Score 815; DB 22; Length 161;

Best Local Similarity 98.8%; Pred. No. 6. 2e-78;

Matches 158; Conservative 1; Mismatches 1;

Indels 0; Gaps 0;

Oy 3 RGCLCLOGSSLISLIVSFLVGAQNSFROEVGAATGAVVGGVAGOLFQKGSGRVAMAIAGA 62

Db 2 RGCLCLOGSSLISLIVSFLVGAQNSFROEVGAATGAVVGGVAGOLFQKGSGRVAMAIAGA 62

Oy 63 GGGLGSKIGOSMDODDKIKLNQSEKVKAGQTWRNRPDTGNNSYSEPVRTYORYNKOER 122

Db 62 GGGLGSKIGOSMDODDKIKLNQSEKVKAGQTWRNRPDTGNNSYSEPVRTYORYNKOER 122

Oy 123 RQQYCREFQQAKMAGOKOETIYTACQPDGKQVISTEK 162

Db 122 RQQYCREFQQAKMAGOKOETIYTACQPDGKQVISTEK 162

RESULT 5

AAU97868

ID AAU97868 standard: Protein: 161 AA.

XX

DE

AAU97868;

XX

DT

12-AUG-2002 (first entry)

XX

DE

Escherichia coli codon optimised Ospa, 17e2.

XX

KW

Outer surface lipoprotein; Ospa; antibacterial; immunosuppressive;

KW

vaccine; poikilothermic fish; fin-fish; Rickettsial septicæmia;

KW

Rickettsial disease; 17e2.

XX

OS

*Piscirickettsia salmonis*.

OS

Synthetic.

XX

PN

CA2339327-A1.

XX

PD

15-MAR-2002.

XX

PF

19-MAR-2001; 2001CA-2339327.

XX

PR

15-SEP-2000; 2000US-0677374.

XX

FA

(THOR,) THORNTON J C.

PA

(KAYW,) KAY W W.

PA

(BURJ,) BURIAN J.

PA

(KUZY,) KUZYK M A.

XX

PI

Thornton JC,

PA

(KAYW,) KAY W W,

PA

(BURJ,) BURIAN J.

PA

(KUZY,) KUZYK M A.

XX

PI

Thornton JC,

PA

(KAYW,) KAY W W,

PA

(BURJ,) BURIAN J.

PA

(KUZY,) KUZYK M A.

XX

PT

Thornton JC,

PA

(KAYW,) KAY W W,

PA

(BURJ,) BURIAN J.

PA

(KUZY,) KUZYK M A.

XX

PT

Thornton JC,

PA

(KAYW,) KAY W W,

PA

(BURJ,) BURIAN J.

PA

(KUZY,) KUZYK M A.

XX

PT

WPI: 2001-31684/34.

DR

N-PSDB; ABK86247.

XX

PT

Inducing immunity in fin fish to Rickettsial septicæmia, comprises

PT administration of an outer surface lipoprotein (Ospa) of a bacterial  
 PT strain, as a vaccine -  
 XX

PS Example 4; Fig 5; 55pp; English.

CC The invention describes a method of protecting a poikilothermic fish  
 CC comprising administering either intraperitoneally by immersion or  
 orally, an immunogenic amount of principal antigen, the Ospa (outer  
 surface lipoprotein), its variants, non-lipidated form or antigenic  
 peptides derived or synthesized with or without an adjuvant. The new  
 method is used to provide an outer surface lipoprotein (Ospa) of  
 bacterial strain *Piscirickettsia salmonis* as a vaccine to induce immunity  
 in fin-fish against Rickettsial septicæmia and other related  
 Rickettsial diseases caused by either a virus, bacteria or parasite.  
 This is the amino acid sequence of the *Escherichia coli* codon optimised  
 outer surface lipoprotein Ospa (17e2) used in the creation of the vaccine  
 described in the invention.

SQ Sequence 161 AA:

```

Query Match 97.5%; Score 815; DB 23; Length 161;
Best Local Similarity 98.8%; Pred. No. 5.2e-78; Matches 1; Mismatches 1; Indels 0; Gaps 0; CQ
  3 RGCLOGSSLITISVFLVGCAONFSRQEYGAATGAWGVGGAGQLEFGKGSGRVAMAIGAVL 62
  2 RGCLOGSSLITISVFLVGCAONFSRQEYGAATGAWGVGGAGQLEFGKGSGRVAMAIGAVL 61

```

QY - 63 GGLIGSKIGOSMDQDKIKLNQSLERKVAGQVTRWRNPDTGNSYSVEPVRTYQRYNQER 122
 Db 62 GGLIGSKIGOSMDQDKIKLNQSLERKVAGQVTRWRNPDTGNSYSVEPVRTYQRYNQER 121
 .123 RQCRCREFQQKAMIAQOKOEIYGTAACPQDPGRWQVISTER 162
 Db 122 RQCRCREFQQKAMIAQOKOEIYGTAACPQDPGRWQVISTER 161

RESULT 6

AABB1128
 ID AABB1128 standard; Protein: 256 AA.

XX AAC
 XX AAAB1128;

XX DT 11-JUL-2001 (first entry)

DE C17E2 Ospa construct with N-terminal fusion partner.

KW Poikilothermic fish; *Piscirickettsia salmonis*; rickettsial pathogen;  
 KW vaccine; Ospa; Salmonid rickettsial septicæmia; rickettsial disease;  
 KW SRS; 17E2; fusion construct.

OS *Piscirickettsia salmonis*.

OS Synthetic.

XX

FH Key Location/Qualifiers
 1..95 /label= Undefined\_N-terminal\_fusion\_partner
 96..256 /label= C17E2\_Ospa
 /note= "Product of Ospa gene optimised for expression in

PN Escherichia coli;" CA2281913-A1.

XX PR 17-SEP-1999; 99CA-2281913.

XX PA (KAYW/) KAY W W.

PA (BURI/) BURIAN J.

---

PA (KUZY/) KUZYK M A.

XX PI KAY WW, Burian J, Kuzyk MA;

XX DR WPI; 2001-316844/34.

XX DR N-PSDB; AAF86248.

PT Method for protecting poikilothermic fish against salmonid rickettsial  
 PT septicæmia and other rickettsial diseases comprises administering a  
 vaccine containing the Ospa protein of *Piscirickettsia salmonis*.

PS Example 4; Fig 5; 35pp; English.

CC This invention relates to a method for the protection against infection  
 CC of a poikilothermic fish by the bacterial pathogen, *Piscirickettsia*  
 CC *salmonis*. The method comprises administering an immunogenic amount of a  
 CC Ospa in the form of a vaccine. The method is used for protecting animals,  
 CC particularly poikilothermic fish, against the bacterial pathogen  
 CC *P. salmonis*. The method is also useful for protecting against salmonid  
 CC rickettsial septicæmia (SRS) and other rickettsial diseases. The present  
 CC sequence represents the amino acid sequence of C17E2, a *P. salmonis* Ospa  
 CC construct optimised for expression in *Escherichia coli*, fused to an  
 CC undefined N-terminal fusion partner. The fusion protein is used in a  
 XX vaccine to create an anti-Ospa antibody response.

SQ Sequence 256 AA:

```

Query Match 97.5%; Score 815; DB 22; Length 256;
Best Local Similarity 98.8%; Pred. No. 1.1e-77; Matches 1; Mismatches 1; Indels 0; Gaps 0; CQ
  3 RGCLOGSSLITISVFLVGCAONFSRQEYGAATGAWGVGGAGQLEFGKGSGRVAMAIGAVL 62
  Db 97 RGCLOGSSLITISVFLVGCAONFSRQEYGAATGAWGVGGAGQLEFGKGSGRVAMAIGAVL 156

```

QY - 63 GGLIGSKIGOSMDQDKIKLNQSLERKVAGQVTRWRNPDTGNSYSVEPVRTYQRYNQER 122
 Db 157 GGLIGSKIGOSMDQDKIKLNQSLERKVAGQVTRWRNPDTGNSYSVEPVRTYQRYNQER 216
 .123 RQCRCREFQQKAMIAQOKOEIYGTAACPQDPGRWQVISTER 152
 Db 217 RQCRCREFQQKAMIAQOKOEIYGTAACPQDPGRWQVISTER 256

RESULT 7

AAU97869
 ID AAU97869 standard; Protein: 256 AA.

XX AAC
 XX AAU97869;

XX DT 12-AUG-2002 (first entry)

DE C17E2 Ospa construct with N-terminal fusion peptide.

KW Outer surface lipoprotein; Ospa: antibacterial; immunosuppressive;  
 KW vaccine; Poikilothermic fish; fin-fish; Rickettsial septicæmia;  
 KW Rickettsial disease; 17e2.

OS *Piscirickettsia salmonis*.

OS Synthetic.

XX CA2339327-A1.

XX PR 15-SEP-2000; 2000US-0677374.

XX PA (THOR/) THORNTON J C.

PA (KAYW/) KAY W W.

PA (BURI/) BURIAN J.

PA (KUZY/) KUZYK M A.  
 XX  
 PI Thornton JC, Kay WW, Burian J, Kuzyk MA;  
 XX  
 DR WPI; 2002-455221/49.  
 XX N-PSDB; ABK52403.  
 XX PT Inducing immunity in fin fish to Rickettsial septicaemia, comprises  
 PT administration of an outer surface lipoprotein (Ospa) of a bacterial  
 PT strain, as a vaccine -  
 XX PS Example 4; Fig 5; 55pp; English.  
 XX  
 CC The invention describes a method of protecting a poikilothermic fish  
 CC against infection by the bacterial pathogen *Piscirickettsia salmonis*  
 CC comprising administering either intraperitoneally, by immersion or  
 orally, an immunogenic amount of principal antigen, the Ospa (outer  
 CC surface lipoprotein), its variants, non-lipidated form or antigenic  
 CC peptides derived or synthesized with or without an adjuvant. The new  
 CC method is used to provide an outer surface lipoprotein (Ospa) of  
 CC bacterial strain *Piscirickettsia salmonis* as a vaccine to induce immunity  
 CC in fin-fish against *Rickettsial* septicemia and other related  
 CC Rickettsial diseases caused by either a virus, bacteria or parasite.  
 CC This is the amino acid sequence of the *Escherichia coli* codon optimised  
 CC outer surface lipoprotein Ospa (17e2) with an N-terminal fusion used in  
 CC the creation of the vaccine described in the invention.  
 XX SQ Sequence 256 AA;

Query Match 97.5%; Score 815; DB 23; Length 256;

Best Local Similarity 98.8%; Pred No 1; 1e-77; Matches 158; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query 3 RGCLQGSSLITISVFLVGCAQNSFRCQEVGAATGAVWGVAGOLFRGSGRVAAMAIGAVL 62  
 Db 97 RGCLQGSSLITISVFLVGCAQNSFRCQEVGAATGAVWGVAGOLFRGSGRVAAMAIGAVL 156

Query 63 GGLIGSIIQGSNDQIKLNUOSLERKVKGAVTRWNPDGNSYSEPVRYQRNQER 122  
 Db 157 GGLIGSIIQGSNDQIKLNUOSLERKVKGAVTRWNPDGNSYSEPVRYQRNQER 216

Query 123 RQYCRCBQQKAMIQOKQEQYTGACRQPDRWRQVISTEK 162  
 Db 217 RQYCRCBQQKAMIQOKQEQYTGACRQPDPGRWVISTER 256

RESULT 8  
 AAB81130  
 ID AAB81130 standard; Peptide: 20 AA.

AAB81130;  
 AC  
 XX DT 11-JUL-2001 (first entry)  
 XX DE OSPA B-cell epitope peptide #2.

XX  
 KW Poikilothermic fish; *Piscirickettsia salmonis*; rickettsial pathogen;  
 KW vaccine; Ospa; salmonid rickettsial septicemia; rickettsial disease;  
 SRS; antibody.  
 OS *Piscirickettsia salmonis*.  
 XX PN CA2281913-A1.

XX  
 PD 17-MAR-2001.  
 XX PF 17-SEP-1999; 99CA-2281913.

XX PR 17-SEP-1999; 99CA-2281913.  
 PA (KAYW/) KAY W W.  
 PA (BURI/) BURIAN J.  
 PA (KUZY/) KUZYK M A.

XX PI Thornton JC, Kay WW, Burian J, Kuzyk MA;  
 XX DR WPI; 2002-455221/49.  
 XX PT Inducing immunity in fin fish to Rickettsial septicaemia, comprises  
 PT administration of an outer surface lipoprotein (Ospa) of a bacterial  
 PT strain, as a vaccine -  
 XX PS Example 2; Page 17; 55pp; English.

XX  
 XX PI Kay WW, Burian J, Kuzyk MA;  
 XX DR WPI; 2001-316844/34.  
 XX PT Method for protecting poikilothermic fish against salmonid rickettsial  
 PT septicemia and other rickettsial diseases comprises administering a  
 PT vaccine containing the Ospa protein of *Piscirickettsia salmonis* -  
 XX PS Example 2; Page 17; 35pp; English.  
 XX  
 CC This invention relates to a method for the protection against infection  
 CC of a poikilothermic fish by the bacterial pathogen, *Piscirickettsia*  
 CC *salmonis*. The method comprises administering an immunogenic amount of a  
 CC Ospa, in the form of a vaccine. The method is used for protecting animals,  
 CC particularly poikilothermic fish, against the bacterial pathogen  
 CC *P. salmonis*. The method is also useful for protecting against salmonid  
 CC rickettsial septicemia (SRS) and other rickettsial diseases. The present  
 CC sequence represents an immunogenic epitope of the *P. salmonis* Ospa  
 CC protein. The peptide is used to raise rabbit anti-Ospa antibodies.  
 XX SQ sequence 20 AA;  
 Query Match 13.4%; Score 112; DB 22; Length 20;  
 Best Local Similarity 100.0%; Pred No. 5.9e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 110 PURTYQNYRKERRQQCRE 129  
 Db 1 PURTYQNYRKERRQQCRE 20

RESULT 9  
 AAU97871  
 ID AAU97871 standard; Peptide: 20 AA.

XX AC AAU97871;  
 XX DT 12-AUG-2002 (first entry)

XX DE Outer surface lipoprotein Ospa based peptide #2.

XX Outer surface lipoprotein; Ospa; antibacterial; immunosuppressive;  
 KW vaccine; poikilothermic fish; fin-fish; Rickettsial septicemia;  
 Rickettsial disease.

XX OS *Piscirickettsia salmonis*.  
 OS Synthetic.

XX PN CA2339327-A1.

XX PD 15-MAR-2002.

XX PP 19-MAR-2001; 2001CA-2339327.

XX PR 15-SEP-2000; 2000US-0677374.

XX PA (THOR/) THORNTON J C.  
 PA (KAYW/) KAY W W.

PA (BURI/) BURIAN J.  
 PA (KUZY/) KUZYK M A.

XX PI Thornton JC, Kay WW, Burian J, Kuzyk MA;

XX DR WPI; 2002-455221/49.

XX PT Inducing immunity in fin fish to Rickettsial septicaemia, comprises  
 PT administration of an outer surface lipoprotein (Ospa) of a bacterial  
 PT strain, as a vaccine -  
 XX PS Example 2; Page 17; 55pp; English.

CC  
XX  
PA (AVET ) AVENTIS PASTEUR LTD.  
XX  
PT Loosmore S, Wang J, Bradley B, Ochs M, Yang Y;  
XX  
DR WPI; 2002-401721/43.  
XX  
DR N-PSDB; RAL46497.

Moraxella polypeptide and polynucleotides useful as vaccine for immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria

The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen *Piscirickettsia salmonis* comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the Ospa (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (Ospa) of bacterial strain *Piscirickettsia salmonis* as a vaccine to induce immunity in fin-fish against Rickettsial septicæmia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This sequence represents a synthetic peptide used to create polyclonal rabbit antibodies against the *Piscirickettsia salmonis* outer surface lipoprotein, Ospa.

XX SQ Sequence 20 AA;

Query Match 13.4%; Score 112; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5, 9e-05;  
Matches 20; Conservative 0; Mismatches 0;  
Indels 0; Gaps 0;

Qy 110 PVRTQYRNYKERRQRCRE 129

Db 1 PVRTQYRNYKERRQRCRE 20

RESULT 10

AA01765 standard; Protein: 197 AA.  
XX  
AC ^AA01765;  
XX  
DT 19-JUL-2002 (first entry)

DE M catarrhialis MCA100414 protein SEQ ID NO: 10.  
XX  
KW Moraxella; vaccine; respiratory tract infection; antiinflammatory;  
KW auditory; antibacterial; otitis media; sinusitis; pneumonia.  
OS Moraxella catarrhialis.  
PN WO200218595-A2.

XX PD 07-MAR-2002.  
XX PF 28-AUG-2001; 2001WO-CA01221.  
XX PR 28-AUG-2000; 2000US-228294P.  
PR 28-AUG-2000; 2000US-228295P.  
PR 28-AUG-2000; 2000US-228296P.  
PR 29-AUG-2000; 2000US-228438P.  
PR 29-AUG-2000; 2000US-228440P.  
PR 29-AUG-2000; 2000US-228441P.  
PR 29-AUG-2000; 2000US-228442P.  
PR 29-AUG-2000; 2000US-228443P.  
PR 29-AUG-2000; 2000US-228511P.  
PR 29-AUG-2000; 2000US-228512P.  
PR 29-AUG-2000; 2000US-228742P.  
PR 29-AUG-2000; 2000US-228773P.  
PR 01-SEP-2000; 2000US-229465P.  
PR 01-SEP-2000; 2000US-229474P.  
PR 01-SEP-2000; 2000US-229475P.  
PR 01-SEP-2000; 2000US-229478P.  
PR 05-SEP-2000; 2000US-229740P.  
PR 05-SEP-2000; 2000US-229803P.  
PR 05-SEP-2000; 2000US-229804P.  
PR 05-SEP-2000; 2000US-229805P.  
PR 05-SEP-2000; 2000US-229806P.  
PR 05-SEP-2000; 2000US-229809P.  
PR 05-SEP-2000; 2000US-229811P.  
PR 06-SEP-2000; 2000US-230214P.  
PR 06-SEP-2000; 2000US-230250P.  
PR 06-SEP-2000; 2000US-230252P.

XX SQ Sequence 197 AA;

Query Match 12.9%; Score 108; DB 23; Length 197;  
Best Local Similarity 32.4%; Pred. No. 0.0038; Mismatches 35; Indels 24; Gaps 5;  
Matches 36; Conservative 16; Mismatches 35; Indels 24; Gaps 5;

Qy 8 GSSLITISVTVGCAONFSRQEVGAATG-----AVVGGVAGOLFKGSGRVAMAIGG 59  
Db 7 QVVLASSMALAGCANTGT----TGNCIGFGGANVNKAIVAGAVAL--GGTAISKAGG 60

Qy 60 -----AVLGLIGSKIGQSNDDQDKIKLNOSLEVKVAGSVTRWRNPDGN 104  
Db 61 EKTGRDAILGAVGAAAGAYMERQK---QIEQQMQGIGWTVTHDIDGN 107

RESULT 11

AAB20105 ID AAB20105 standard; Protein: 224 AA.  
XX  
AC AAB20105;  
XX DT 23-APR-2001 (first entry)  
XX DE Moraxella catarrhialis BASEB13 protein.  
XX KW BASEB13; infection; otitis media; pneumonia; therapy; diagnosis;  
KW antibacterial; antimicrobial.  
OS Moraxella catarrhialis.  
PN WO200100836-A1.  
XX PD 04 - JAN - 2001.  
XX PR 23-JUN-2000; 2000WO-EP05851.  
XX PR 25-JUN-1999; 99GB-001504.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PT Thonnard J;  
XX DR WPI; 2001-112458/12.  
XX N-PSDB; AAF30043.

New BASEB13 polypeptide isolated from *Moraxella catarrhialis* bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia

PT  
XX  
PS Claim 1; Page 67; 86pp; English.

XX CC The present sequence is that of BASEB13 protein from *Moraxella catarrhialis* strain MC2931 (ATCC 43617), a causative agent of otitis

CC media in children and pneumonia in adults. The invention provides  
 CC BASB13 polypeptides, and poly nucleotides encoding them as well as  
 CC expression vectors, host cells and methods for producing BASB13  
 CC polypeptides using recombinant methods. Also claimed is a vaccine  
 CC composition comprising a BASB13 polypeptide, or a polypeptide having at least  
 CC 85% amino acid sequence identity to BASB13, or comprising a  
 CC polynucleotide encoding such a polypeptide. A claimed method of  
 CC diagnosing a Moraxella infection involves identifying a BASB13  
 CC polypeptide or antibody. A claimed therapeutic composition useful  
 CC in treating humans with *M. catarrhalis* infection comprises at least  
 CC 1 antibody directed against a BASB13 polypeptide. BASB13  
 CC polypeptides also have utility in raising specific antibodies,  
 XX and in screening for antibacterial drugs.

SQ Sequence 224 AA:  
 XX

Query Match 12.9%; Score 108; DB 22; Length 224;  
 Best Local Similarity 32.4%; Pred. No. 0033; Mismatches 35; Indels 24; gaps 5;  
 Matches 36; Conservative 16; Mismatches 35; Indels 24; gaps 5;  
 Oy 8 GSSLITISVFLVGCAQNSRSQEVGATG-----AVVSGVAGQLFGKGSGRVAMIGG 59  
 Db 7 GVVLLASSMALAGCAGTGT---TGAGTGEGGANVNVKAIVAGAVAL---GGTAISKATGG 60  
 Oy 60 -----AVLGLIGSISIGQSDQQDKIKUNSLQEVKAQGQVTPRWNPDGN 104  
 Db 61 EKTGRDAILGAVGAAAGAYMEROAK---QIEQDMQGTVTVDIDTGN 107

RESULT 12

ID AAY34487 standard; Protein: 223 AA.  
 XX  
 AC AAY34487;  
 DT 25-AUG-1999 (first entry)

XX DE Porphorymonas gingivalis protein PG3.  
 DE KW 'Porphorymonas gingivalis'; PG; periodontal disease; gingivitis;  
 KW vaccine; antigenic.  
 XX OS Porphorymonas gingivalis.  
 OS PN WO9929870-A1.  
 PN XX PD 17-JUN-1999.  
 PD XX PF 10-DEC-1998; 98AU-AU01023.  
 XX PR 04-AUG-1998; 98AU-0005028.  
 PR 04-AUG-1998; 98AU-0005039.  
 PR 31-DEC-1997; 97AU-0001182.  
 PR 30-JAN-1998; 98AU-0001545.  
 PR 10-MAR-1998; 98AU-0002264.  
 PR 09-APR-1998; 98AU-0002911.  
 PR 23-APR-1998; 98AU-0003128.  
 PR 05-MAY-1998; 98AU-0003348.  
 PR 22-MAY-1998; 98AU-0003654.  
 PR 29-JUL-1998; 98AU-0004917.

RESULT 13

ID AAY34362 standard; Protein: 230 AA.  
 XX  
 AC AAY34362;  
 DT 25-AUG-1999 (first entry)  
 DE Porphorymonas gingivalis protein PG3.  
 DE KW Porphorymonas gingivalis; PG; periodontal disease; gingivitis;  
 KW vaccine; antigenic.  
 XX OS Porphorymonas gingivalis.  
 OS PN WO9929870-A1.  
 PN XX PD 17-JUN-1999.  
 PD XX PF 10-DEC-1998; 98AU-AU01023.  
 XX PR 04-AUG-1998; 98AU-0005028.  
 PR 10-DEC-1997; 97AU-0000339.  
 PR 31-DEC-1997; 97AU-0001182.  
 PR 30-JAN-1998; 98AU-0001546.  
 PR 09-APR-1998; 98AU-0002264.  
 PR 23-APR-1998; 98AU-003128.  
 PR 05-MAY-1998; 98AU-0003348.  
 PR 22-MAY-1998; 98AU-0003654.  
 PR 29-JUL-1998; 98AU-0004917.

PS Claim 1; Page 469; 58pp; English.  
 XX  
 CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic  
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAY34318 to  
 CC AAY3483. AAX91802 to AAX9198 represent PCR primers used in the  
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial  
 CC activity with a vaccine mechanism of action. The PG polypeptides can be  
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can  
 CC be used to detect Porphyromonas gingivalis in standard hybridisation  
 CC assays. Porphyromonas gingivalis is involved in periodontal disease  
 CC especially gingivitis.

SQ Sequence 223 AA:

Query Match 12.6%; Score 105.5; DB 20; Length 223;  
 Best Local Similarity 36.1%; Pred. No. 0061; Mismatches 31; Indels 3; Gaps 2;  
 Matches 26; Conservative 12; Mismatches 31; Indels 3; Gaps 2;  
 Oy 9 SLLITISVFLVGCAQNSRSQEVGATG-----AVVSGVAGQLFGKGSGRVAMIGG 67  
 Db 8 ASVLASALVFAGCGLN-NMAKGGLTGAGYGAIGAGVGNVAGNTAVGAIVWGGAAG 65  
 Oy 68 SKIGOSMDOK 79  
 Db 66 ALIGKRMKDQR 77

PT Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;  
 PT Ross BC, Rotheil LJ, Webb EA;  
 XX WPI: 1999-385613/32.  
 DR N-PSDB: AAY91705.  
 XX PT Antigenic Porphyromonas gingivalis peptides for preventing  
 PT gingivitis  
 XX

PS AAX91536 to AAX91801 encode two hundred and sixty six antigenic  
 XX

Porphyromonas gingivalis (PG) polypeptide sequences given in AAY134318 to AAY134583. AAX9102 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphyromonas gingivalis. Probes can be used to detect Porphyromonas gingivalis in standard hybridisation assays. Porphyromonas gingivalis is involved in periodontal disease especially gingivitis.

X  
Q Sequence 230 AA;

	Best Local Similarity	Pct. Mismatches	Indels	Gaps
Matches	39.0%	0.0%	23	0
21; Conservative	9			
Qy	30	VGAATGAVVGGAGOLFKGSSGRVAMAIGVAVLGLGSKIGSMDQDKKL	82	
:    :    :    :    :    :    :    :    :    :    :    :				
Db	62	VGTLLGGCALGCGIAGSTIGGRGQATAAVVGAAGGAIAGSKIEKMSQNGAEL	114	
RESULT	15			
ABG15906				
ID	ABG15906	standard; protein;	309 AA.	
xx				

Query Match	12.6%	Score 105.5;	DB 20;	Length 230;
Best Local Similarity	36.1%	Pred. No. 0	0 0063;	Gaps
Matches	26;	Conservative	12;	Mismatches 31; Indels 3;
YY	9	SLLIIISVFLGCCAQNSFRQEVGAATGAVWGGVAGQLFGKGSGRVAM-AIGAVVGLLIG	67	
bb	15	ASVLAYALVFRGCGLN--NMAKGGGLIGAGYVGAGAIGAG3VGVNAGNTAVGAIWGTAVGGAG	72	
DY	68	SKIGQSMQDQDK	79	
Db	73	ALIGKMDQDK	84	

<p>Best Local Matches 21; Similarity 39.6%; Freq. No. 0.0001; Mismatches 23; Indels 0; Gaps 0; O.</p>	<p>QY 30 VGAATGAVVGGVAGOLFKGKSSGRVAMAIGGANVLGLGLSKIGSQMDQDKIKL 82                :   :   :   :   :   :   :   :   :   :   :   :            Db 62 WGTLLGGCALGGIAGSTIGGRRQATAAVVGAIGGAAGSKIEEKKMSQVNGAEL 114       </p>
<p>RESULT 15</p>	
<p>ABC15906</p>	
<p>ID ABC15906 standard; Protein: 309 AA.</p>	
<p>XX</p>	
<p>AC ABC15906;</p>	
<p>XX</p>	
<p>DT 18-FEB-2002 (first entry)</p>	
<p>XX</p>	
<p>DE Novel human diagnostic protein #15897.</p>	
<p>XX</p>	
<p>DE Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.</p>	
<p>KW Homo sapiens.</p>	
<p>XX</p>	
<p>OS WO2001175067-K2.</p>	
<p>XX</p>	
<p>PN PD 11-OCT-2001.</p>	

	ID	AAR05799	standard; Protein; 154 AA.	
	DE	XX		
	AC	XX		
	XX	XX		
	DT	31-AUG-1990	(first entry)	
	XX	XX		
	XX	XX	PBOMP-2 gene prod.	
	DE	XX	outer membrane proteins; PBOMP-2; immunisation;	
	KW	XX	Praxis Biologics Outer Membrane Protein.	
	OS	XX	Haemophilus influenzae.	
	XX	XX	WO9002557-A.	
	PD	22-MAR-1990.		
	XX	XX		
	PF	31-AUG-1989;	89WO-US03779.	
	XX	XX	01-SEP-1988;	88US-0239572.
	PR	XX	21-AUG-1989;	89US-0396572.
	CC	XX	(PRAK-) PRAXIS BIOLICS IN.	
	CC	XX	Anilionis A, Seid RC, Deich RA, Zlotnick GW, Green BA;	
	CC	XX	PT	
	CC	XX	PT Anilionis A, Seid RC, Deich RA, Zlotnick GW, Green BA;	
	CC	XX	PT	
	CC	XX	WPI; 1990-115815/15.	
	CC	XX	N-PSPB; AAQ03870.	
	CC	XX		
	CC	XX	Outer membrane protein epitopes of Haemophilus influenzae- used in	
	CC	XX	PT prodn. of antibodies, in vaccines and for prodn. of reagents for	
	CC	XX	PT diagnosis.	
	CC	XX	WPI; 1990-115815/15.	
	CC	XX	N-PSPB; AAQ03870.	
	CC	XX		
	CC	XX	Disclosure; Fig 15; 164pp; English.	
	CC	XX	The PBOMP proteins were isolated from a PBOMP-enriched insoluble	
	CC	XX	cell wall fraction from physically disrupted cells of <i>H. influenzae</i>	
	CC	XX	and then solubilizing the PBOMP from the cell wall fraction by heating	
	CC	XX	in the presence of a detergent or digesting the cell wall fraction	
	CC	XX	with lysozyme, opt. in the presence of a detergent. The genes	
	CC	XX	encoding the PBOMP proteins were isolated by screening a DNA library	
	CC	XX	with an oligonucleotide probe based on the amino acid sequence of the	
	CC	XX	PBOMP protein, or using antibodies to PBOMP.	
SQ	Sequence	154 AA;	12.2%; score 102; DB 11; Length 154;	
Query Match				
Best Local Similarity		11.7%; Score 98; DB 22; Length 309;		
Matches		34.0%; Pred. No. 0.057; 39; Indels 14; Gaps 33; Conservative 11; Mismatches 11;		

Thu Feb 13 14:53:25 2003

us-09-677-374-2.rag

Page 9

Qy 13 IISVFLVGCAGNFSR---QEVGATGAVVGGVAGOLFCKG--SGRVAMAIGGAVLGGI 65  
| | : | ; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 185 IISILPAKAVADNSQNKRNAQAFGALIGAVAGGVIGHNVGSGSNSTAGAVGGAVGAA 244  
Qy 66 IGSKI-----GOHQDQPKIKLUQSLEVKVAGOT 95  
| | : | | ; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 245 AGSMWNDKTLMEGVSILTYKEGTKVITSTOVNGKEFPT 281

Search completed: February 12, 2003, 16:43:14  
Job time : 38 secs

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Db 491 QGAGAAAAGQGEGIRGQGAGQQGGYGLGSQGSRGGLGGAGAAAAGAGQGG 550 ;  
 Qy 65 LIGSKIGO 72 ;  
 Db 551 LGQQGAGQ 558 ;

RESULT 2  
 US-09-47-806-1  
 ; Sequence 1, Application US/09247806  
 ; Patent No. 628047  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PHILIPPE, Michel  
 ; APPLICANT: GARRON, Jean-Claude  
 ; TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT  
 ; TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN  
 ; FILE REFERENCE: 6308-03655-0  
 ; CURRENT APPLICATION NUMBER: US/09/247,806  
 ; CURRENT FILING DATE: 1999-02-11  
 ; EARLIER APPLICATION NUMBER: FR 98/01614  
 ; EARLIER FILING DATE: 1998-02-11  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SEQ ID NO 1  
 ; LENGTH: 651  
 ; TYPE: PRT  
 ; ORGANISM: Nephila clavipes  
 ; US-09-47-806-1

Query Match 9.7%; Score 81.5; DB 4; Length 651;  
 Best Local Similarity 36.8%; Pred. No. 0.91; Matches 25; Conservative 3; Mismatches 17; Indels 23; Gaps 2;

Qy 28 QEVGAATGAVWG---GVAGQ-----LFGKGSSGRVAMIAQAVLGG 64 ;  
 Db 491 OGAGAAAAAVAGQECIRGOCAGQGGYGGLGSOGSRRGGLGQAGAAAAGAGQGG 550 ;  
 Qy 65 LIGSKIGO 72 ;  
 Db 551 LGQQGAGQ 558 ;

RESULT 3  
 US-08-425-069-2  
 ; Sequence 2, Application US/08425069  
 ; General Information:  
 ; APPLICANT: Lewis, Randolph V.  
 ; APPLICANT: Xu, Ming  
 ; TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK  
 ; TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL  
 ; TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF  
 ; NUMBER OF SEQUENCES: 62  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
 ; STREET: 301 No. 598994th Washington Street  
 ; CITY: Falls Church  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22046  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/317,844B  
 ; FILING DATE: 04-OCT-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Murphy Jr., Gerald M  
 ; REGISTRATION NUMBER: 28,977  
 ; REFERENCE/DOCKET NUMBER: 1447-105P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 241-1300  
 ; TELEX: 248345  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 718 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-425-069-2

Query Match 9.7%; Score 81.5; DB 2; Length 718;

Best Local Similarity 36.8%; Pred. No. 1; Mismatches 17; Indels 23; Gaps 2; Matches 25; Conservative 3; Mismatches 17; Indels 23; Gaps 2;

Query Match 9.7%; Score 81.5; DB 3; Length 747;

Best Local Similarity 36.8%; Pred. No. 1.1; Mismatches 17; Indels 23; Gaps 2; Matches 25; Conservative 3; Mismatches 17; Indels 23; Gaps 2;

Query 28 QEVGAATGAVVG---GVAGO-----LFGKGSGRVMAIGAVLGG 64  
 Db 491 OCAGAAAAAVGAGQEGIRGOGAGGGYGLGSQSGRGGLGQAGAAAAGGAGGG 550  
 Qy 65 LGSKIGQ 72  
 Db 551 LGQQAGQ 558

RESULT 5  
 US-09-034-177-3 Application US/09034177  
 Sequence 3, Application US/09034177  
 Patent No. 6127146  
 GENERAL INFORMATION:  
 APPLICANT: Lal, Pretel  
 APPLICANT: Guebler, Karl J.  
 APPLICANT: Corley, Neil C.  
 TITLE OF INVENTION: HUMAN FIBROUS PROTEIN  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSCF FOR Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/034,177  
 FILING DATE: 9/1/03  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE DOCKET NUMBER: PF-0486 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELIX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 747 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: GI 117414  
 US-09-034-177-3

Query Match 9.3%; Score 78; DB 1; Length 865;  
 Best Local Similarity 25.4%; Pred. No. 3.3; Mismatches 30; Indels 28; Gaps 7; Matches 36; Conservative 30; Mismatches 48; Indels 28; Gaps 7;

Query 17 ELVGCQNFSSQ-EVGAATGAVVGAGQEGIRGOGAGGGYGLGSQSGRGGLGQAGAAAAGGAGGG 67  
 Db 688 FMNGLAELFNGMGOVQGAIGKVVAANGAIVSTISGVSAFMNSPREGALAGLITIAGLVA 747  
 Qy 68 SKIGOSMDQDKIKLN----QSLEKVGQYWRWNIDTGNSYVSVERTORYINKO 120  
 Db 748 AFL-ARYNNKKLPKALYPMTTEVLA-QATRELIGEESDD----LERTSID 796  
 CLONE: GI 117414  
 US-09-034-177-3

Query Match 9.7%; Score 81.5; DB 3; Length 747;  
 Best Local Similarity 36.8%; Pred. No. 1.1; Mismatches 17; Indels 23; Gaps 2; Matches 25; Conservative 3; Mismatches 17; Indels 23; Gaps 2;

Query 28 QEVGAATGAVVG---GVAGO-----LFGKGSGRVMAIGAVLGG 64  
 Db 491 OCAGAAAAAVGAGQEGIRGOGAGGGYGLGSQSGRGGLGQAGAAAAGGAGGG 550  
 Qy 65 LGSKIGQ 72  
 Db 551 LGQQAGQ 558

RESULT 6  
 US-07-803-633A-13  
 Sequence 13, Application US/07803633A  
 Patent No. 5569025  
 GENERAL INFORMATION:  
 APPLICANT: NAZERIAN, Keyvan  
 APPLICANT: LEE, Lucy F.  
 APPLICANT: YANAGIDA, No. 5369025oru  
 APPLICANT: OGAWA, Ryohel  
 APPLICANT: LI, Yi  
 TITLE OF INVENTION: RECOMBINANT FOWLPox VACCINE FOR PROTECTION AGAINST MAREK'S DISEASE  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
 STREET: 301 NO. 5369025th Washington Street  
 CITY: Falls Church  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22040-0747  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/803,633A  
 FILING DATE: 1/9/12/10  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Murphy Jr., Gerald M.  
 REGISTRATION NUMBER: 28, 977  
 REFERENCE DOCKET NUMBER: 1644-103P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 241-1300  
 TELEX: (703) 241-2848  
 FAX: 248345  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 865 amino acids  
 TYPE: AMINO ACID  
 TOROLOGY: linear  
 MOLECULE TYPE: protein

US-07-803-633A-13

Query Match 9.3%; Score 78; DB 1; Length 865;  
 Best Local Similarity 25.4%; Pred. No. 3.3; Mismatches 30; Indels 28; Gaps 7; Matches 36; Conservative 30; Mismatches 48; Indels 28; Gaps 7;

Query 17 ELVGCQNFSSQ-EVGAATGAVVGAGQEGIRGOGAGGGYGLGSQSGRGGLGQAGAAAAGGAGGG 67  
 Db 688 FMNGLAELFNGMGOVQGAIGKVVAANGAIVSTISGVSAFMNSPREGALAGLITIAGLVA 747  
 Qy 68 SKIGOSMDQDKIKLN----QSLEKVGQYWRWNIDTGNSYVSVERTORYINKO 120  
 Db 748 AFL-ARYNNKKLPKALYPMTTEVLA-QATRELIGEESDD----LERTSID 796  
 CLONE: GI 117414  
 US-09-034-177-3

Query Match 9.7%; Score 81.5; DB 3; Length 747;  
 Best Local Similarity 36.8%; Pred. No. 1.1; Mismatches 17; Indels 23; Gaps 2; Matches 25; Conservative 3; Mismatches 17; Indels 23; Gaps 2;

Query 28 QEVGAATGAVVG---GVAGO-----LFGKGSGRVMAIGAVLGG 64  
 Db 491 OCAGAAAAAVGAGQEGIRGOGAGGGYGLGSQSGRGGLGQAGAAAAGGAGGG 550  
 Qy 65 LGSKIGQ 72  
 Db 551 LGQQAGQ 558

RESULT 7  
 US-09-553-498-B  
 Sequence 8, Application US/09553498  
 Patent No. 6309861  
 GENERAL INFORMATION:  
 APPLICANT: Ambrosius, Dorothée  
 APPLICANT: Ambrosius, Rudolph, Rainer  
 APPLICANT: Schaeffner, Jeorg  
 APPLICANT: Schwarz, Elisabeth  
 TITLE OF INVENTION: Process for the production of naturally folded and secreted pr  
 FILE REFERENCE: Case 20379

CURRENT FILING DATE: 2000-04-20  
; PRIORITY FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO: 8  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: E. coli  
; US-09-553-498-8

Query Match 9 3%; Score 77.5; DB 4; Length 255;  
; Best Local Similarity 20.9%; Pred. No. 0.73; Mismatches 37; Conservative 28; Indels 31; Gaps 7;  
; Matches 37; Conserving 28; Mismatches 37;

Qy 6 LQGSSLLIISVFVLCGAQNSFQEVGAATGAW--GGVAGOLFKGKSGSRVAMIGAV 61  
; Db 83 LQMTSLRSIDTAMYCCARDYQAY-WGQGTIVTWSGGGGSGGGGGSDIELIQSPA 141  
; Qy 62 LGGLIGSKIGQSMQDQDKR-LN-----QSLEKVKAGOYTRWRNPDTNSY 106  
; Db 142 MSASPGKEVITMCSASSSVRYMWNFQOKSGTSPKRWVDTSSLSSGVPARFSGSGCTSY 201  
; Qy 107 SVEPVRTYQRYNQKERRQRQYCRPQQKAMT-RGQKQOLYGACRQPDPGRWQVSTE 161  
; Db 202 SL---TISSEMEAADATYYCQOWSSNPLTFAGTAKLKLRAAEQ---KLISEE 249

RESULT 8  
; US-09-618-869-8  
; sequence: 8, Application US/09618869  
; GENERAL INFORMATION:  
; PATENT NO.: 645579  
; APPLICANT: Ambrosius, Dorthee  
; APPLICANT: Rudolph, Rainer  
; APPLICANT: Schaeffner, Joerg  
; APPLICANT: Schwarz, Elisabeth  
; TITLE OF INVENTION: PROCESSES FOR THE PRODUCTION OF NATURALLY FOLDED AND SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR CHAPERONES  
; FILE REFERENCE: 20381  
; CURRENT APPLICATION NUMBER: US/09/618-869  
; CURRENT FILING DATE: 2000-07-19  
; PRIORITY APPLICATION NUMBER: EP99114811.5  
; PRIORITY FILING DATE: 1999-07-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 8  
; LENGTH: 255  
; ORGANISM: Escherichia coli

Query Match 9 3%; Score 77.5; DB 4; Length 255;  
; Best Local Similarity 20.9%; Pred. No. 0.73; Mismatches 37; Conservative 28; Indels 31; Gaps 7;  
; Matches 37; Conserving 28; Mismatches 37;

Qy 6 LOGSSLLIISVFVLCGAQNSFQEVGAATGAW--GGVAGOLFKGKSGSRVAMIGAV 61  
; Db 83 LQMTSLRSIDTAMYCCARDYQAY-WGQGTIVTWSGGGGSGGGGGSDIELIQSPA 141  
; Qy 62 LGGLIGSKIGQSMQDQDKR-LN-----QSLEKVKAGOYTRWRNPDTNSY 106  
; Db 142 MSASPGKEVITMCSASSSVRYMWNFQOKSGTSPKRWVDTSSLSSGVPARFSGSGCTSY 201  
; Qy 107 SVEPVRTYQRYNQKERRQRQYCRPQQKAMT-RGQKQOLYGACRQPDPGRWQVSTE 161  
; Db 202 SL---TISSEMEAADATYYCQOWSSNPLTFAGTAKLKLRAAEQ---KLISEE 249

RESULT 9  
; US-09-677-351-2  
; Sequence 2, Application US/09067351  
; General Information:  
; Patent No. 5994081  
; General Information:  
; Applicant: Tang, Y. Tom  
; Applicant: Hillman, Jennifer L.  
; Applicant: Corley, Neil C.  
; Applicant: Baughn, Mariah  
; Title of Invention: HUMAN KERATINS  
; Number of Sequences: 6  
; Correspondence Address:  
; Street: 3174 PORTER DRIVE  
; City: PALO ALTO  
; State: CALIFORNIA  
; Country: USA  
; Zip: 94304  
; Computer Readable Form:  
; Medium Type: Floppy disk  
; Computer: IBM PC compatible  
; Operating System: PC-DOS/MS-DOS  
; Software: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; Current Application Data:  
; Application Number: US/09/0677,351  
; Filing Date: Herewith  
; Classification:  
; Attorney/Agent Information:  
; Name: Cerrone, Michael C.  
; Registration Number: 39,132  
; Reference Docket Number: PF-0511 US  
; Telephone: (650) 855-0555  
; Telecommunication Information:  
; Telefax: (650) 847-4166  
; Information for Seq ID No: 2:  
; Sequence Characteristics:  
; Length: 551 amino acids  
; Type: amino acid  
; Strandness: single  
; Topology: linear  
; Immediate Source:  
; Library: KERANOT02  
; Clone: 2029050

RESULT 10  
; US-09-360-490-2  
; Sequence 2, Application US/09360490  
; General Information:  
; Patent No. 6221843  
; General Information:  
; Applicant: Tang, Y. Tom  
; Applicant: Hillman, Jennifer L.  
; Applicant: Corley, Neil C.  
; Applicant: Baughn, Mariah  
; Title of Invention: HUMAN KERATINS  
; Number of Sequences: 6  
; Correspondence Address:  
; Street: 3174 PORTER DRIVE

CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/360,490  
 APPLICATION NUMBER: US/09/360,490  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 09/067,351  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GERRONE, MICHAEL C.  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PP-0511 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 351 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: KERANOTO2  
 CLONE: 2029060  
 ;US-09-360-490-2

Query Match 9.2%; Score 77; DB 4; Length 551;  
 Best Local Similarity 22.4%; Pred. No. 2.3; Mismatches 53; Indels 16; Gaps 2;  
 Matches 28; Conservative 28; Mismatches 53; Indels 16; Gaps 2;

Qy 8 GSSLILISVVLVGCGNFSRQEVGATGAVVGGVAGQLFGKGSGRGRVAMAIGGAVGAVGLIG 67  
 Db 54 GASFCRSRSLVNLGGAKRVSLSNGCSCRSQFGGRASNGCGVNSG--FEGYGGVGGFSG 110

Qy 68 SK-----IGQSADQQDKIKLNLKNSLEKKAQGVTWRNRNPDTGNSYSEPVRY 114  
 Db 111 PSFPVCPGGIQEVTVNQSLITPLHLQDPTIQRVRAEREQIKTLNNKFTSPIDKVFL 170

Qy 115 QRYNK 119  
 Db 171 EQONK 175

RESULT 11  
 US-09-374-077C-2  
 ; Sequence 2, Application US/08374077C  
 ; Patent No. 6027912  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hall, Linda M.  
 ; APPLICANT: Ren, Delian  
 ; APPLICANT: Zheng, Wei  
 ; APPLICANT: Dubald, Manuel Marcel Paul  
 ; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel  
 ; NUMBER OF SEQUENCES: 101  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP  
 ; STREET: 699 Prince Street  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22314-3187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/895,590  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/374,888  
 FILING DATE: 19-JAN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McGowan, Malcolm M.  
 REGISTRATION NUMBER: 39,300  
 REFERENCE/DOCKET NUMBER: 022650-264  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEX/FAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2516 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ;US-08-374-077C-2

Query Match 9.2%; Score 76.5; DB 3; Length 2516;  
 Best Local Similarity 24.8%; Pred. No. 20; Mismatches 66; Indels 13; Gaps 4;  
 Matches 32; Conservative 18; Mismatches 66; Indels 13; Gaps 4;

Qy 30 VGAATGCAVVGCGAVQGLFGKGSGRGRVAMAIGG-AVILGGLGSKIGQS---MDQODKIKLN 83  
 Db 2389 IGSSNSIPIGSAGGLGGAGGGVG-GLGGSIRNAFGGSSGPSSLSPOHQYSGTIN 2447

Qy 84 -----OSLERVKAGQVTRNRNPDTGNSYSEPVRYQYRYNKOERQQCREFQOKAMIA 137  
 Db 2448 SPPIDPNRLERPVATVTTNNKNSQVSONNNSLNVRNANSQNMSPTCQPVQQSQLR 2507

Qy 138 GQOKOETYG 146  
 Db 2508 GQGNOTYSS 2516

RESULT 12  
 US-08-895,590-2  
 ; Sequence 2, Application US/08895590  
 ; Patent No. 6307410  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hall, Linda M.  
 ; APPLICANT: Ren, Delian  
 ; APPLICANT: Zheng, Wei  
 ; APPLICANT: Dubald, Manuel Marcel Paul  
 ; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel  
 ; NUMBER OF SEQUENCES: 101  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP  
 ; STREET: 699 Prince Street  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22314-3187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/895,590  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/374,888  
 FILING DATE: 19-JAN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McGowan, Malcolm M.  
 REGISTRATION NUMBER: 39,300  
 REFERENCE/DOCKET NUMBER: 022650-263  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2516 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-895-590-2

Query Match 9.2%; Score 76.5; DB 4; Length 2516;  
 Best Local Similarity 24.8%; Pred. No. 20;  
 Matches 32; Conservative 18; Mismatches 66; Indels 13; Gaps 4;  
 Best Local Similarity 24.8%; Pred. No. 20;  
 Matches 32; Conservative 18; Mismatches 66; Indels 13; Gaps 4;

QY 30 VGGATGAVVGGVAGQLFGKGSKRGRVAMAIGG---AVLGGLGSKIGS---MDQQDKIKLN 83  
 Db 2389 IGSSNGSISFGSGAGGLGGAGSGGGV-GLGSSSIRNAFGGSGSGPSSLSPHQPSGTLN 2447  
 QY 84 -----QLEKVKAGQYTRWRNPDGTGSYSVPEVRTQRYNKQERIQCYCBEFQKAMIA 137  
 Db 2448 SPPPIPDRNLRRVATVTNNNNKSQVSNQNSSSLNVRANANSONQNMSPTGQPVQQQSPLR 2507  
 QY 138 GQKQEYGT 146  
 Db 2508 GQGNQTYSS 2516

RESULT 13  
 US-09-539-879A-2  
 Sequence 2, Application US/09539879A  
 Patent No. 6436627  
 GENERAL INFORMATION:  
 APPLICANT: Hall, Linda M.  
 Ren, Dejian  
 Zheng, Wei  
 Dubald, Manuel Marcel Paul  
 TITLE OF INVENTION: Genes Encoding an Invertebrate Alpha<sub>1</sub>  
 Calcium Channel Subunit  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 ADDRESS: BURNS, DOANE, SWEKKER & MATHIS, LLP  
 STREET: 699 Prince Street  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22314-3187  
 CURRENT APPLICATION DATA:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.30  
 APPLICATION NUMBER: US/09/539, 879A  
 FILING DATE: 31-Mar-2000  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/111, 865  
 FILING DATE: <unknown>  
 APPLICATION NUMBER: US 08/374, 077  
 FILING DATE: 19-JAN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McGowan, Malcolm M.  
 REGISTRATION NUMBER: 39,300  
 REFERENCE/DOCKET NUMBER: 022650-264  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2516 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-910-760-12

RESULT 14  
 US-07-910-760-12  
 Sequence 12, Application US/0910760  
 Patent No. 5683864  
 GENERAL INFORMATION:  
 APPLICANT: Houghton, Michael  
 APPLICANT: Choo, Qui-Lim  
 TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV) Antisera for Anti-HCV Antibodies  
 TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV) Antisera for Use in Immunoassays  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Chiron Corporation  
 STREET: P.O. Box 8097 (Int. Prop. R-440)  
 CITY: Emeryville  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 94662-8097  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/910, 760  
 FILING DATE: 07-JUL-1992  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Blackburn Esq., Robert P.  
 REGISTRATION NUMBER: 30,447  
 REFERENCE/DOCKET NUMBER: 0101.002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 601-2702  
 TELEFAX: (510) 655-3542  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1021 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-910-760-12

Query Match 9.1%; Score 76; DB 1; Length 1021;  
 Best Local Similarity 20.9%; Pred. No. 6,8;  
 Matches 42; Conservative 24; Mismatches 63; Indels 72; Gaps 9;

QY 31 GAATGAVVGGVAGQLGK--GSGRVAMAIGG---GGAVLGLGSKR---GSMQDKIKLN 83  
 Db 792 GATAFVGAGLAGAATGSGVGLGKVLDILAGYAGVAGLVAFKIMSGEVPTSDLVNL 851  
 QY 84 QSL-----EKVKAGQ-VTRWRN----PDGTGSYSVPEVRTQRYNKQ 120  
 Db 852 PAILSPGALGVWGVCAATIRRHHGPGCAGVWMPNTTAKSPCHVSPNSCPNCPVWVQ 111

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-539-879A-2

RESULT 15  
 US-08-440-519-12  
 Sequence 12, Application US/08440519  
 ;  
 Patent No. 5712087,  
 GENERAL INFORMATION:  
 ;  
 APPLICANT: Houghton, Michael  
 APPLICANT: Cho, Qui-Lin  
 APPLICANT: Kuo, George  
 TITLE OF INVENTION: Combinations of hepatitis C virus (HCV)  
 TITLE OF INVENTION: Antigens for use in immunoassays for Anti-HCV Ant.  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Chiron Corporation  
 STREET: P.O. Box 8097 (Int. Prop. R-440)  
 CITY: Emeryville  
 STATE: CA  
 COUNTRY: U.S.A.  
 Z.FP: 94662-8097  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 ;  
 APPLICATION NUMBER: US/08/440,519  
 FILING DATE: 12-MAY-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/910,760  
 REFERENCE/DOCKET NUMBER: 0101.002  
 TELECOMMUNICATION INFORMATION:  
 ;  
 TELEPHONE: (510) 601-2702  
 TELEFAX: (510) 655-3442  
 INFORMATION FOR SEQ ID NO: 12:  
 ;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 103 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ;  
 US-08-440-519-12

Query Match 9.1%; Score 76; DB 1; Length 1021;  
 Best Local Similarity 20.9%; Pred. No. 6.8; Gaps  
 Matches 42; Conservative 24; Mismatches 63; Indels 72; Gaps  
 Oy 31 GAATGATGGVAGVAGLGLFGK-GSGRYAMAI--GCAVLGLIGLSKI-GSMDQDKIKLN 83  
 Db 792 GAATRFGVAGLAGAIGSVGLGKVLDIAGYGVAGVALVAKIMSGEVPSDETDLVNL 851  
 Oy 84 OSL--EKRVAQO-VTRWRN---PDTENSYSVEPPVRYQRYKQ 120  
 Db 852 PAILSPGALWVGWVCAAILRRHVGPGEGAWOMNRLIAFASRGHNVSPCGNNSTNPKPORK 911  
 Oy 121 ERRO-----OCREFOOKAMPAQKOEIYGFA 148  
 Db 912 NKRNTNRQDVKPGGGQIVGGVYLLPRGRPLGVRAKTRKTSESRQPRGRROPI-PKA 969  
 Oy 149 RQPDR-----WQVISTE 161  
 ;|:|||

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PRIOR APPLICATION NUMBER: 60/253, 625  
 PRIORITY FILING DATE: 2000-11-27  
 PRIORITY APPLICATION NUMBER: 60/257, 931  
 PRIORITY FILING DATE: 2000-12-22  
 PRIORITY APPLICATION NUMBER: 60/269, 308  
 PRIORITY FILING DATE: 2001-02-16  
 NUMBER OF SEQ ID NOS: 14110  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 12113  
 LENGTH: 514  
 TYPE: PRT  
 ORGANISM: *Pseudomonas aeruginosa*  
 US-09-815-242-12113

Query Match 9.2%; Score 76.5; DB 10; Length 514;  
 Best Local Similarity 27.8%; Pred. No. 4.5;  
 Matches 37; Conservative 18; Mismatches 47; Indels 31; Gaps 7;

QY 20 GCAQNFNSRQEVAAGTAVVGGVAGQFLGKSGGRVAMAIGGAVVGLGLISKGQSADQQDK 79  
 Db 62 GMALNALEQDSVGAVLGEYOGCLAEGNKAATGTRILEVPVGPPELLGRVVDALGNPDPGKGP 121

QY 80 I--KLNOSEKVKGQVTRWRNPDTGNSYSV-EPRY-T-YORYNKQERRQQYCREFQQKAM 135  
 Db 122 IDAKAIDAVERKAPSVI--WRK-----SVDQPVQTGYKSVD-----AM 157

QY 136 I---ACQOKEIYG 145  
 Db 158 IPVGRCQRELLIG 170

RESULT 6  
 US-09-738-626-5811  
 Sequence 5811, Application US/09738626  
 Publication No. US20020197605A1  
 GENERAL INFORMATION:  
 APPLICANT: NAKAGAWA, SATOSHI  
 APPLICANT: MIZOGUCHI, HIROSHI  
 APPLICANT: ANDO, SEIKO  
 APPLICANT: HAYASHI, MIKIRO  
 APPLICANT: OCHIAI, KEIKO  
 APPLICANT: YOKOI, HARUHICO  
 APPLICANT: TATEISHI, NAOKO  
 APPLICANT: SENOH, AKIHIRO  
 APPLICANT: IKEDA, MASATO  
 APPLICANT: OZAKI, AKITO  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-125  
 CURRENT APPLICATION NUMBER: US/09/738, 626  
 CURRENT FILING DATE: 2000-12-18  
 PRIORITY APPLICATION NUMBER: JP 99/377484  
 PRIORITY FILING DATE: 1999-12-16  
 PRIORITY APPLICATION NUMBER: JP 00/159162  
 PRIORITY FILING DATE: 2000-04-07  
 PRIORITY APPLICATION NUMBER: JP 00/280988  
 PRIORITY FILING DATE: 2000-08-03  
 NUMBER OF SEQ ID NOS: 7059  
 SOFTWARE: PatentIn ver. 3.0  
 SEQ ID NO 5811  
 LENGTH: 346  
 TYPE: PRT  
 ORGANISM: *Corynebacterium glutamicum*  
 US-09-738-626-5811

Query Match 9.1%; Score 76; DB 9; Length 346;  
 Best Local Similarity 28.8%; Pred. No. 3.1; Matches 21; Conservative 8; Mismatches 36; Indels 8; Gaps 1;

QY 4 GCLQGSSLITISVFLVGCAQNFNSRQEVAAGTAVVGGVAGQFLGKSGGRVAMAIGGAVVGLGLISKGQSADQQDK 55  
 Db 98 GVSASSGLGVAVTIVGTVLGSASASIGVIGAFAFGVGAVALATMVSRGVQGGSSTVV 157

QY 56 ATGGAVLGGLIGS 68

---

Db 158 ILAGVAVAFAFSS 170

RESULT 7  
 US-09-815-242-12104  
 Sequence 12104, Application US/09815242  
 Patent No. US2002061569A1  
 GENERAL INFORMATION:  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari L.  
 APPLICANT: Zyskind, Judith W.  
 APPLICANT: Wall, Daniel  
 APPLICANT: Carr, Grant J.  
 APPLICANT: Yamamoto, Robert T.  
 APPLICANT: Xu, H. Howard  
 TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes  
 FILE REFERENCE: ELITRA.01A  
 CURRENT APPLICATION NUMBER: US/09/815, 242  
 CURRENT FILING DATE: 2001-03-21  
 PRIORITY APPLICATION NUMBER: 60/191, 078  
 PRIORITY FILING DATE: 2000-03-21  
 PRIORITY APPLICATION NUMBER: 60/206, 848  
 PRIORITY FILING DATE: 2000-05-23  
 PRIORITY APPLICATION NUMBER: 60/207, 727  
 PRIORITY FILING DATE: 2000-05-26  
 PRIORITY APPLICATION NUMBER: 60/242, 578  
 PRIORITY FILING DATE: 2000-10-23  
 PRIORITY APPLICATION NUMBER: 60/253, 625  
 PRIORITY FILING DATE: 2000-11-27  
 PRIORITY APPLICATION NUMBER: 60/257, 931  
 PRIORITY FILING DATE: 2000-12-22  
 PRIORITY APPLICATION NUMBER: 60/269, 308  
 PRIORITY FILING DATE: 2001-02-16  
 NUMBER OF SEQ ID NOS: 14110  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 12104  
 LENGTH: 342  
 TYPE: PRT  
 ORGANISM: *Pseudomonas aeruginosa*  
 US-09-815-242-12104

Query Match 9.0%; Score 75; DB 10; Length 342;  
 Best Local Similarity 24.0%; Pred. No. 3.8; Matches 25; Conservative 18; Mismatches 25; Indels 36; Gaps 4;

QY 27 RQEVGATGAVVGGVAGQFLGKSGGRVAMAIGGAVVGLGLISKGQSADQQDK 68  
 Db 231 QRDIGGAHGVLTAVNSARSQAGMARRGGTIALVGLPPCDFPTPIFDVLKGHLIAGS 290

QY 69 KIGQSMQDQDKI-----KLNOSEKVKGQV 94  
 Db 291 IVGTRADQELDFAGEGLVVKATHPGKLDIDINQILDQMRAQGI 334

RESULT 8  
 US-09-978-295A-28  
 Sequence 28, Application US/09978295A  
 Patent No. US20020156006A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyer, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.



PRIOR FILING DATE: 1998-05-05 ;  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06 ;  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William T.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PC27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 03/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1991-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1991-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/07910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107

Query Match 8.9%; Score 74.5; DB 9; length 285;  
Best Local Similarity 20.8%; Pred. No. 3,4; DB 9;  
Matches 26; Conservative 27; Mismatches 49; Indels 23; Gaps 4;

Oy 12 IILSVF-LVGCQNEFSRQEVAATGAWGGYAGOLRGKGSGRVAMIGGAVLGLGLGSKI 70  
Db 144 VFTVTTTNTNTSLNVRNKKDALSHFVITAGAVGVLGSRL-----RINTVGLRAGGIGALL 198  
Oy 71 GOSMD-----QQDKIKLNQSLERVKVAGQVTRRNPPDTGNNSVSEPVRYOR 116  
Db 199 GTPVGGLUMAFQKYAGETVQERKOKDRKALHELK--LEEWKGRLQVTEHLPEKLESSR 255  
Oy 117 YNKQE 121  
Oy :::::  
Db 256 EDEPE 260

RESULT 9  
US-09-978-697-28  
; Sequence 28, Application US/09978697  
; Patent No. US2002016928A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter

PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080370  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083550  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30

APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kijavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James;  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2630R1C9

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/911585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062449

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/063311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/063364

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PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

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PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078004

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PRIOR APPLICATION NUMBER: 60/078866

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PRIOR APPLICATION NUMBER: 60/078939

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PRIOR APPLICATION NUMBER: 60/078936

PRIOR FILING DATE: 1998-03-25

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PRIOR FILING DATE: 1998-03-26

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PRIOR FILING DATE: 1998-04-01

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PRIOR APPLICATION NUMBER: 60/081838

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PRIOR FILING DATE: 1998-04-22

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PRIOR APPLICATION NUMBER: 60/083558

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083559

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083560

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083742

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PRIOR FILING DATE: 1998-04-30 ; APPLICANT: Gao, Wei-Qiang  
; PRIOR APPLICATION NUMBER: 60/081366 ; APPLICANT: Gerber, Hansperter  
; PRIOR FILING DATE: 1998-05-05 ; APPLICANT: Gerritsen, Mary E.  
; PRIOR APPLICATION NUMBER: 60/084414 ; APPLICANT: Goddard, Audrey  
; PRIOR FILING DATE: 1998-05-06 ; APPLICANT: Godowski, Paul J.  
; PRIOR APPLICATION NUMBER: 60/084441 ; APPLICANT: Grimaldi, J. Christopher  
; PRIOR FILING DATE: 1998-05-06 ; APPLICANT: Gurney, Austin L.  
; PRIOR APPLICATION NUMBER: 60/084637 ; APPLICANT: Hillan, Kenneth J.  
; PRIOR FILING DATE: 1998-05-07 ; APPLICANT: Kljavin, Iva J.  
; PRIOR APPLICATION NUMBER: 60/084639 ; APPLICANT: Kuo, Sophia S.  
; PRIOR FILING DATE: 1998-05-07 ; APPLICANT: Napier, Mary A.  
; PRIOR APPLICATION NUMBER: 60/084640 ; APPLICANT: Pan, James  
; PRIOR FILING DATE: 1998-05-07 ; APPLICANT: Paoni, Nicholas F.  
; PRIOR APPLICATION NUMBER: 60/084643 ; APPLICANT: Roy, Margaret Ann  
; PRIOR FILING DATE: 1998-05-07 ; APPLICANT: Shelton, David L.  
; PRIOR APPLICATION NUMBER: 60/084650 ; APPLICANT: Stewart, Timothy A.  
; PRIOR FILING DATE: 1998-05-07 ; APPLICANT: Tumas, Daniel  
; PRIOR APPLICATION NUMBER: 60/084627 ; APPLICANT: Williams, P. Mickey  
; PRIOR FILING DATE: 1998-05-13 ; APPLICANT: Wood, William I.  
; PRIOR APPLICATION NUMBER: 60/084628 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; PRIOR FILING DATE: 1998-05-13 ; FILE REFERENCE: P2630PIC63  
; PRIOR APPLICATION NUMBER: 60/085339 ; CURRENT APPLICATION NUMBER: US/09/999 832A  
; PRIOR FILING DATE: 1998-05-13 ; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: 60/085338 ; PRIOR APPLICATION NUMBER: 09/918585  
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; PRIOR APPLICATION NUMBER: 60/080105 ; PRIOR APPLICATION NUMBER: 60/080105

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RESULT 11

US-09-999-832A-28

Sequence 28, Application US/0999832A

Publication No. US0020192706A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman







RESULT 15  
 US-10-175-737-4  
 ; Sequence 4, Application US/10175737  
 ; Publication No. US20030013153A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnyer, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3430RIC50  
 CURRENT APPLICATION NUMBER: US/10/175,737  
 CURRENT FILING DATE: 2002-06-19  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 612  
 SEQ ID NO 4  
 LENGTH: 285  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-10-175-737-4

Query Match 8.9%; Score 74.5; DB 9; Length 285;  
 Best Local Similarity 20.8%; Pred. No. 3.4;  
 Matches 26; Conservative 27; Mismatches 49; Indels 23; Gaps 4;

QY 12 IISVF-LVGCQNFSSQEVGAATGAVVGGVAGQLGGKGSGSRVAMAIGGAVLGGGLGSKI 70  
 Db 144 VFTVIFTWNTSLNVRNKDALSHFVITAGAVTGSFLF----RINVGLRLGVAGGIIGALL 198  
 QY 71 GOSMD-----QDKIKLNQSLERKVKAQCVTRRNPDGNSISVEPVTYQR 116  
 Db 199 GTPVGGILMARAOKYAGETVQERKQKAKHIELK--LEENGRGLOVTEHPEKEFESSLR 255  
 QY 117 YNKQE 121  
 Db 256 EDEPE 260

Search completed: February 12, 2003, 16:50:27  
 Job time : 13 secs

Copyright (c) 1993 - 2003 Compugen Ltd.	GenCore version 5.1.3
Run on: February 12, 2003, 16:41:16 ; Search time 40 Seconds	(without alignments)
Scoring table: BLOSUM62	834.491 Million cell updates/sec
Searched: 671580 seqs, 206047115 residues	
Total number of hits satisfying chosen parameters: 671580	
Minimum DB seq length: 0	
Maximum DB seq length: 0	
Post-processing: Maximum Match 0%	
Listing first 45 summaries	
Database : SPTREMBL_21:	
1: sp-archaea:*	
2: sp-bacteria:*	
3: sp-fungi:*	
4: sp-human:*	
5: sp-invertebrate:*	
6: sp-mammal:*	
7: sp-mhc:*	
8: sp-organelle:*	
9: sp-phage:*	
10: sp-plant:*	
11: sp-protoct:*	
12: sp-virus:*	
13: sp-vertebrate:*	
14: sp-unclassified:*	
15: sp-virus:*	
16: sp-bacteriip:*	
17: sp-archeap:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Score
1	836
2	313.5
3	291
4	266.5
5	260.5
6	259.5
7	252
8	247
9	247
10	237.5
11	237.5
12	236.5
13	223.5
14	143
15	167
16	131.5
17	130.5
18	128.5
19	125.5
20	116
21	112
22	112
23	111.5
24	111
25	110.5
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27	108.5
28	107.5
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31	105.5
32	106
33	105.5
34	105.5
35	102
36	102
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39	99.5
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43	99
44	98
45	98
ALIGMENTS	
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ID Q9F9K8	PRELIMINARY;
ID Q9F9K8;	PRT; 162 AA.
AC Q9F9K8;	
DT 01-MAR-2001 (TREMBLrel: 16, Created)	
DT 01-MAR-2001 (TREMBLrel: 16, Last sequence update)	
DT 01-MAR-2001 (TREMBLrel: 16, Last annotation update)	
DE 17 kDa antigen.	
GN OSPA.	
OS Piscirickettsia salmonis.	
OC Bacteria; Proteobacteria; gamma subdivision; Piscirickettsia group; Piscirickettsiia; NCBI_TaxID:1238;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN:LF-89;	
RA Kuzuyi M.A., Burian J., Thornton J.C., Kay W.W.;	"Identification of a genus common Rickettsial surface antigen in the salmonid pathogen Piscirickettsia salmonis.";
RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.	
RL EMBL; AR184152; ARGI1000.1; -;	
DR SEQUENCE FROM N.A.	
DR AR184152; ARGI1000.1; -;	
DR SEQUENCE 162 AA; 17661 MW; DDE9B6FD94A527E CRC64;	
Query SEQUENCE	Match
Best Local Similarity	100.0% ; Score 836; DB 2; Length 162;
Matches	162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MNRCGCGSSLLISVFLVGCAONFSRQEVGATGAVVGGAGOLFCKGSERVAMIGGA
Db	1 MNRCGCGSSLLISVFLVGCAONFSRQEVGATGAVVGGAGOLFCKGSERVAMIGGA
QY	61 VIGGLGSKGSMDDDKIKINQSLKVKAGCVRTRNNPFGNSVSEPRPTYQYNQ
Db	61 VIGGLGSKGSMDDDKIKINQSLKVKAGCVRTRNNPFGNSVSEPRPTYQYNQ
QY	121 ERQQYKREPQKAMIAQKQDYEYGATCQPOCRWQISTEK
Db	121 ERQQYKREPQKAMIAQKQDYEYGATCQPOCRWQISTEK
Q8vue8 brucella ab	09AGC7





Db 125 QD----CRVYTQTVVIGGKQOKAYGNACRQPDCQ 154

RESULT 9

Q9F9Q9 PRELIMINARY; PRT; 151 AA.

ID Q9F9Q9; 01-MAR-2001 (TREMBrel. 16, Created)

ID DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)

ID DT 01-MAR-2001 (TREMBrel. 16, Last annotation update)

DE Outer membrane protein (Fragment).

OS Rickettsia helvetica.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI\_TAXID=35789;

RN [1]

SEQUENCE FROM N.A.

RA Nilsson K., Pahlson C.; "Novel peptide diagnostic reagent and kit for detection of rickettsiosis"; Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF181036; AXG09427.1; -.

FT NON\_TER 151 151

SQ SEQUENCE 151 AA; 15621 MW; B7740B9C71E4B39 CRC64;

Query Match 29.5%; Score 247; DB 2; Length 151; Best Local Similarity 36.2%; Pred. No. 7.8e-15; Matches 55; Conservative 26; Mismatches 57; Indels 14; Gaps 4;

QY 9 SSITISV--FLWGC--AQNFSSRQEVAAGCAVGAVGQFLGKGSSGRVAMAIGAVLG 63

Db 5 SKIMIALALAASMLQACNCPGGMKKQGTGTLGGAGGLGSQFGKGKGQLVGVGGALLG 64

QY 64 GLIGSKIGQSMQDK---IKLNQSLKEVRAQVTRWRNDTGSYSVERVYQRYNK 119

Db 65 AVLGGQTIVAGMDEQDRRLAELTSQRALEAAPSGSNTEWRNPFDNGNYVTPNKTY--- 119

QY 120 QERRQQCREFQQKAMAGQKOEITGACROP 151

Db 120 RNSTGQCREYTOTVVIGGKQOKAYGNACROP 151

RESULT 10

Q9F0Q1 PRELIMINARY; PRT; 131 AA.

ID Q9F0Q1; 01-MAR-2001 (TREMBrel. 15, Created)

ID DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)

ID DT 01-MAR-2001 (TREMBrel. 16, Last annotation update)

DE 17 kDa protein (Fragment).

OS Rickettsia sp. California 2.

OC Rickettsiaceae; Rickettsiae; Rickettsiales;

OX NCBI\_TAXID=147259;

RN [1]

SEQUENCE FROM N.A.

RC Raoult D.; "A new SFG rickettsia isolated from fleas."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

RC STRAIN=CALIFORNIA 2.

RP SEQUENCE FROM N.A.

RC Roux V.; Raoult D.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF210693; AAG6854.1; -.

FT NON\_TER 1 1

FT NON\_TER 131 131

SQ SEQUENCE 131 AA; 13374 MW; 23C881B29FFP860 CRC64;

Query Match 28.4%; Score 237.5; DB 2; Length 131; Best Local Similarity 37.8%; Pred. No. 4.7e-14; Matches 48; Conservative 22; Mismatches 48; Indels 9; Gaps 2;

QY 26 SROEVGAATGAVVGGVAGQFLGKGSSGRVAMAIGAVLGIGLGSKIGQSMQDK---IK 81

Db 10 NKQGTGTLGGAGGALLGSQFGKGKGQLVGVGGALLGAVLGGQICAGMDSDRRAELT 69

QY 82 LNSQLEKKVAGQVTRWRNDTGSYSVERVYQRYNKQERQQYREFQQKAMAGQK 141

Db 70 SORALEAAPSGSNTEWRNPFDNGNYVTPNKTY---RNSTGQCREYTOTVVIGKQ 124

QY 142 ETIGTAC 148

Db 125 KAYGNAC 131

RESULT 11

QY 26 SROEVGAATGAVVGGVAGQFLGKGSSGRVAMAIGAVLGIGLGSKIGQSMQDK---IK 81

Db 10 NKQGTGTLGGAGGALLGSQFGKGKGQLVGVGGALLGAVLGGQICAGMDSDRRAELT 69

QY 82 LNSQLEKKVAGQVTRWRNDTGSYSVERVYQRYNKQERQQYREFQQKAMAGQK 141

Db 70 SORALEAAPSGSNTEWRNPFDNGNYVTPNKTY---RNSTGQCREYTOTVVIGKQ 124

QY 142 ETIGTAC 148

Db 125 KAYGNAC 131

SEQUENCE FROM N.A.

RA Warren J.H., Hurst G.D., Zhang W., Breeuwer J.A., Strouthamer R.; "Rickettsia relative associated with male killing in the ladybird beetle (*Acalia bipunctata*)"; J. Bacteriol. 176:388-94 (1994).

RL EMBL; U04162; AAA19235.1; -.

FT NON\_TER 1

FT NON\_TER 131 131

SQ SEQUENCE 131 AA; 13344 MW; A1DCF71050DF52DF CRC64;

Query Match 28.4%; Score 237.5; DB 2; Length 131; Best Local Similarity 37.8%; Pred. No. 4.7e-14; Matches 48; Conservative 22; Mismatches 48; Indels 9; Gaps 2;

QY 26 SROEVGAATGAVVGGVAGQFLGKGSSGRVAMAIGAVLGIGLGSKIGQSMQDK---IK 81

Db 10 NKQGTGTLGGAGGALLGSQFGKGKGQLVGVGGALLGAVLGGQICAGMDSDRRAELT 69

QY 82 LNSQLEKKVAGQVTRWRNDTGSYSVERVYQRYNKQERQQYREFQQKAMAGQK 141

Db 70 SORALEAAPSGSNTEWRNPFDNGNYVTPNKTY---RNSTGQCREYTOTVVIGKQ 124

QY 142 ETIGTAC 148

Db 125 KAYGNAC 131

RESULT 12

Q9L522 PRELIMINARY; PRT; 131 AA.

ID Q9L522; 01-OCT-2000 (TREMBrel. 15, Created)

ID DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)

ID DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)

DE 17 kDa surface antigen (Fragment).

OS Rickettsia peacocki.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI\_TAXID=47589;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=DAE100;

RC MEDLINE=21091941; PubMed=11157215;

RA Simser J.A., Palmer A.T., Munderlich U.G., Kurtti T.J.;



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